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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 07:09:40 : Search time 1534 Seconds

(Without alignments)  
8651.160 Million cell updates/sec

Title: US-09-941-042C-1

Perfect score: 456

Sequence: 1 ggaacataatcaatcatt.....ggttaaaagcagttacagag 456

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_pai:\*
- 2: gb\_hlg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
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- 22: em\_ov:\*
- 23: em\_pat:\*
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- 27: em\_sts:\*
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- 40: em\_hlgo\_mus:\*
- 41: em\_hlgo\_other:\*

Pred. No. 18 is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	456	100.0	456	6	AX467562 Sequence
2	456	100.0	1030	6	AR059251 Sequence
3	456	100.0	1294	6	AR059250 Sequence
4	456	100.0	1372	6	AR059249 Sequence
5	456	100.0	1988	6	AR059248 Sequence
6	456	100.0	2010	6	AR059247 Sequence
7	245	53.7	2347	8	TOBSPAEB
8	184.2	40.4	6053	8	NTB82A
9	148	32.5	722	6	AR059252
10	94.4	20.7	5040	8	NSCHRBIB
11	69	15.1	157373	9	AL593856
12	68.8	15.1	116696	3	PPMAL3P3
13	66.8	14.6	150199	9	AC087568
14	66.6	14.6	5145	6	AX281353
15	66.6	14.6	5145	6	AX345250
16	66.4	14.6	8305	6	AX346470
17	65.6	14.4	149497	2	AL627305
18	65.4	14.3	3945	8	AF141654
19	65.2	14.3	234112	3	PPMAL4P2
20	65	14.3	152797	9	AC108052
21	65	14.3	194943	9	AC105252
22	64.8	14.2	101944	9	AC011463
23	64.6	14.2	44067	9	AL357136
24	64.2	14.1	155106	9	AC104069
25	63.8	14.0	195130	9	AL359832
26	63.2	13.9	135711	3	VITVD10
27	63	13.8	124820	2	AC117073
28	63	13.8	158813	9	AC080091
29	62.8	13.8	91798	9	HSK8152G3
30	62.8	13.8	96953	9	AC079621
31	62.6	13.7	145598	9	AC008132
32	62.6	13.7	169541	9	AL136178
33	62.4	13.7	38013	9	AL590287
34	62.4	13.7	110000	2	PPMAL4P1.1
35	62.4	13.7	176368	9	CNS01RGG
36	62.2	13.6	103344	9	HS1100E15
37	62.2	13.6	165260	9	AC024341
38	62.2	13.6	165423	9	CNS07ECV
39	62.2	13.6	224448	2	PPMAL4P4
40	62	13.6	1266	3	DDI301668
41	62	13.6	1792	3	AF151388
42	62	13.6	186431	2	AC022281
43	62	13.6	198853	2	AL365354
44	61.8	13.6	106090	5	AL732577
45	61.8	13.6	167362	2	AC006269

#### ALIGNMENTS

RESULT 1	AX467562	456 bp	DNA	linear	PAT 16-JUL-2002
LOCUS	AX467562	Sequence 1 from Patent WO0218607.			
DEFINITION	AX467562				
ACCESSION	AX467562.1	GI:21900757			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
	common tobacco.				
	Nicotiana tabacum				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
	Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.				
REFERENCE					
AUTHORS	1	Conkling, M.A. and Li, Y.			
TITLE		Transgenic plants containing molecular decoys that alter protein			

content therein  
Patent: WO 0218607-A 1 07-MAR-2002;  
JOURNAL

**NORTH CAROLINA STATE UNIVERSITY (US)**  
**Location/Qualifiers**

source	1. .456
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158 57 56 175 +
/organism="Nicotiana tabacum"
/db_xref="taxon:4097"

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Best Local Similarity	100.0%;	Pred. No. 2.6e-59;		
Matches 456; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

[illegible]

RESULT 2  
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Query Match	100.0%;	Score 456;	DB 6;	length 1030;
Best Local Similarity	100.0%;	Pred. No. 2.1e-59;		
Matches 456; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

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D <b>b</b>	1	GGAAACATTTCCATTGACTTGTAGTTTCCTCCTCAATAACCGTAGAATAACTTTTGCGCTT	60
O <b>y</b>	61	GCTAATAAAGAATACCTTGAAATAGCTTAAGTTAAATATAATAATGACAATAATGATTTTTAGGA	120
D <b>b</b>	61	GCTAATAAAGACTTGAAATAGCTTAAGTTAAATAATAATGACATAATAGATTTTAGGA	120
O <b>y</b>	121	ATTAGATTTTGAGTTTAACTTAACTTATTGACTTGTACAGTTTATATAATTCGAAGGCC	180
D <b>b</b>	121	ATTAGATTTTGAGTTTAACTTAACTTATTGACTTGTACAGTTTATATAATTCGAAGGCC	180
O <b>y</b>	181	ATGAAAAATTTAAAGCTTATTAGCTTTAAACTCTATATAATTTTTCATATGTAAA	240
D <b>b</b>	181	ATGAAAAATTTAAAGCTTATTAGCTTTAAACTCTATATAATTTTTCATATGTAAA	240
O <b>y</b>	241	TTTAATCGGTAGTGCATATTTTTCATTTATTTATATAATAAATAAACCCTAACCT	300
D <b>b</b>	241	TTTAATCGGTAGTGCATATATTTTTCATTTATATAATAAATAAACCCTAACCT	300
O <b>y</b>	301	AATTAATCGGTACAGTTATAGATTTTATATAAAATCCTACGGTCTCAGAGAAGAACTTAA	360
D <b>b</b>	301	AATTAATCGGTACAGTTATAGATTTTATATAAAATCCTACGGTCTCAGAGAAGAACTTAA	360
O <b>y</b>	361	AATCGGTTCGGTGGGACGTTGCGATCGGTAGTTCGATTTTCCAATATTCTTGACACT	420
D <b>b</b>	361	AATCGGTTCGGTGGGACGTTGCGATCGGTAGTTCGATTTTCCAATATTCTTGACACT	420
O <b>y</b>	421	CCTAGTTGTTGTATAGGTAATAAAGCACATTCACAG	456
D <b>b</b>	421	CCTAGTTGTTGTATAGGTAATAAAGCACATTCACAG	456

RESULT 3			
LOCUS	AR059250		
DEFINITION	AR059250	1294 bp	DNA
ACCESSION	Sequence 4 from patent US 5837876.		
VERSION	AR059250		
KEYWORDS	AR059250.1 GI:5984827		
SOURCE	Unknown:		
ORGANISM	Unknown:		
	Unclassified.		
REFERENCE	1 (bases 1 to 1294)		
AUTHORS	Conkling,M.A., Mendu,N. and Song,W.		
TITLE	Root cortex specific gene promoter		
JOURNAL	Patent: US 5837876-A 4 17-NOV-1998;		
FEATURES	location/qualifiers		
source	1..1294		

Query Match	100.0%	Score 456;	DB 6;	Length 1294;
Best Local Similarity	100.0%	Pred. NO. 2e-59;		
Matches 456; Conservative	0;	Mismatches	0;	Gaps 0

QY	1	GGAAACATATTCATACATCTTGTAGTTGGCTACTCATATCGCTAGAAATAGTTGGCCCT	60
Db	265	GGAAACATATTCATACATCTGTAGTTGGCTACTCATATCGCTAGAAATAGTTGGCCCT	324
QY	61	GCTAATAAGATACCTGGAATAGCTTACTTTAAATAATAATAGCAATATAGATTTTAA	120
Db	325	GCTAATAAGATACCTGGAATAGCTTACTTTAAATAATAATAGCAATATAGATTTTAA	384
QY	121	ATTAGTATTTTGAAGTTTAATTACTTATTTAGACTTGTACAGTTTTTTTAATTCGAAGGCC	180
Db	385	ATTAGTATTTTGAAGTTTAAATTACTTATTTAGACTTGTACAGTTTTTTTAATTCGAAGGCC	444
QY	181	ATGAAAAATTTAAAGCTTATTAGTTTAAACTCTATAAATAATTTTCATATGTAA	240
Db	445	ATGAAAAATTTAAAGCTTATTAGTTTAAACTCTATAAATAATTTTCATATGTAA	504
QY	241	TTTATCGGTATTAAGTCGATATTTTTCATATTTTATTAATAAATAAATACTTACCT	300



[illegible]

LOCUS	AR059248	1988 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	Sequence 2 from patent US 5837876.				
ACCESSION	AR059248				
VERSION	AR059248.1	GI:5984825			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1988)				
TITLE	Conkling, M.A., Mendu, N. and Song, W.				
JOURNAL	Root cortex specific gene promoter				
FEATURES	Patent: US 5837876-A 2 17-NOV-1998;				
Source	Location/Qualifiers				
	1..1988				
BASE COUNT	714 a	271 c	302 g	701 t	
ORIGIN	/organism="unknown"				
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Best Local Similarity	100.0%;	Pred. No. 1..e-59;			
Matches 456;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	GGAACCATTCATCATGATGTAGTTGGTACACATATGCGTAGAATACCTTGCCCT	60		
Db	959	GGAACCATTCATCATGATGTAGTTGGTACACATATGCGTAGAATACCTTGCCCT	1018		
QY	61	GCTAATATAAGATCTGTAATAGCTTGTAGTTAATATAATATAGCATATAGATTTTGA	120		
Db	1019	GCTAATATAAGATCTGTAATAGCTTGTAGTTAATATAATATAGCATATAGATTTTGA	1078		
QY	121	ATTAGATTTTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	180		
Db	1079	ATTAGATTTTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1138		
QY	181	ATGAAAAATTTAAGCTTTTATAGTTTAACTACATATATAATTTTCCATATGTAA	240		
Db	1139	ATGAAAAATTTAAGCTTTTATAGTTTAACTACATATATAATTTTCCATATGTAA	1198		
QY	241	TTTATCGGTATAGTTGATTTTTCATTTTCAATTTATTTTATATAATAATAAACTTACCT	300		
Db	1199	TTTATCGGTATAGTTGATTTTTCATTTTCAATTTATTTTATATAATAATAAACTTACCT	1258		
QY	301	AATTATCGGTACAT	360		
Db	1259	AATTATCGGTACAT	1318		
QY	361	AATCGGTGCGTGGGACGGTTCATAGGTTTTCATTAATATATATATATATATATAT	420		
Db	1319	AATCGGTGCGTGGGACGGTTCATAGGTTTTCATTAATATATATATATATATATAT	1378		
QY	421	CCTAGTGTGTTGTATAGTATATAAAAGACGTTACAGAG	456		
Db	1379	CCTAGTGTGTTGTATAGTATATAAAAGACGTTACAGAG	1414		
RESULT 6	AR059247	2010 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR059247				
DEFINITION	Sequence 1 from patent US 5837876.				
ACCESSION	AR059247				
VERSION	AR059247.1	GI:5984824			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 2010)				
TITLE	Conkling, M.A., Mendu, N. and Song, W.				
JOURNAL	Root cortex specific gene promoter				
FEATURES	Patent: US 5837876-A 1 17-NOV-1998;				
Source	Location/Qualifiers				
	1..2010				
	/organism="unknown"				

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Best Local Similarity 100.0%; Pred. No. 1.7e-59;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAACATTTCAATGCTAGTTGCTAGCTACATATCGGTAGATATCTTGTGCTT 60
DB 959 GGAACATTTCAATGCTAGTTGCTAGCTACATATCGGTAGATATCTTGTGCTT 1018
QY 61 GCTAATAAGATAGTGAATAGCTAGTTAAATATAAGCATATAGATTTTGA 120
DB 1019 GCTAATAAGATAGTGAATAGCTAGTTAAATATAAGCATATAGATTTTGA 1078
QY 121 ATTAGTATTTGAGTTAATTTACTTATTTGCTTGAAGTTTATTAATCCAGGCC 180
DB 1079 ATTAGTATTTGAGTTAATTTACTTATTTGCTTGAAGTTTATTAATCCAGGCC 1138
QY 181 ATGAAATTTTATGCTTATTAGTTTAACTTATATATAATTTTCATATGTATAA 240
DB 1139 ATGAAATTTTATGCTTATTAGTTTAACTTATATATAATTTTCATATGTATAA 1198
QY 241 TTTAATCGATAGTTCGATATTTTTCATTTTATTAATAAATAAATTCACCT 300
DB 1199 TTTAATCGATAGTTCGATATTTTTCATTTTATTAATAAATAAATTCACCT 1258
QY 301 AATTATCGTACATATATAGATTTAATAAATCTACGCTTCTCAGAAAGAACTTAA 360
DB 1259 AATTATCGGACAGTATATAGATTTAATAAATCTACGCTTCTCAGAAAGAACTTAA 1318
QY 361 AATCGGTGCGGCGGCGGCTGATCGGTTTGTAGTTCATTAATTCATTTGACACT 420
DB 1319 AATCGGTGCGGCGGCGGCTGATCGGTTTGTAGTTCATTAATTCATTTGACACT 1378
QY 421 CCTAGTGTGTTATAGTAAAAAGCAGTTACAGAG 456
DB 1379 CCTAGTGTGTTATAGTAAAAAGCAGTTACAGAG 1414

RESULT 7
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LOCUS TOBACO psab gene for psi-E subunit of photosystem I, complete
DEFINITION cds.
ACCESSION D42070.1 GI:575606
VERSION D42070.1 GI:575606
KEYWORDS psab; Psi-E subunit of photosystem I.
SOURCE Nicotiana sylvestris (library: lambda DASH) DNA, clone KUEG3.
ORGANISM Nicotiana sylvestris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.
1 (sites)
REFERENCE Kubota,T., Yamamoto,Y.Y. and Obokata,J.
AUTHORS Cloning of a nuclear-encoded photosystem I gene, psab, in
TITLE Nicotiana sylvestris
JOURNAL Plant Physiol. 108 (3), 1297-1298 (1995)
MEDLINE 95357419
REFERENCE 2 (bases 1 to 2347)
AUTHORS Obokata,J.
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 2347)
AUTHORS Obokata,J.
DIRECT SUBMISSION Submitted (09-NOV-1994) Junichi Obokata, Hokkaido University,
Graduate School of Environment, Earth Sci., Kita-ku, Sapporo, Hokkaido
060, Japan (E-mail: joecul.hines.hokudai.ac.jp, Tel:011-706-5291,
Fax:011-757-5994)
FEATURES
Source Location/Qualifiers
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/db_xref="taxon:4096"

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/codon_start=1
/product="Psi-E subunit of photosystem I"
/protein_id="BAA07667.1"
/db_xref="GI:1217601"
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/number=2
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/number=3

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Matches 308; Conservative 0; Mismatches 45; Indels 16; Gaps 2;

QY 1 GGAACATTTCAATGCTAGTTGCTAGCTACATATCGGTAGATATCTTGTGCTT 60
DB 220 GGAACATTTCAATGCTAGTTGCTAGCTACATATCGGTAGATATCTTGTGCTT 279
QY 61 GCTAATAAGATAGTGAATAGCTAGTTAAATATAAGCATATAGATTTTGA 120
DB 280 GCTAATAAGATAGTGAATAGCTAGTTAAATATAAGCATATAGATTTTGA 339
QY 121 ATTAGTATTTGAGTTAATTTACTTATTTGCTTGAAGTTTATTAATCCAGGCC 180
DB 340 ATTAGTATTTGAGTTAATTTACTTATTTGCTTGAAGTTTATTAATCCAGGCC 399
QY 181 ATGAAATTTTATGCTTATTAGTTTAACTTATATATAATTTTCATATGTATAA 240
DB 400 AAGAAATTTTATGCTTATTAGTTTAACTTATATATAATTTTCATATGTATCAT 459
QY 241 TTTAATCGTATAGTTCGATATTTTTCATTTTATTAATAAATAAATTCACCT 300
DB 460 TTTAA-----ATTATTCGATTTATTTTATTAATAAATAAATTCACCT 504
QY 301 AATTATCGTACATATATAGATTTAATAAATCTACGCTTCTCAGAAAGAACTTAA 359
DB 505 AATTATCGGCGGCTTATATATATTAATAAATCTACGCTTCTCAGAAAGAACTTAA 564
QY 360 AATCGGTT 368
DB 565 AATCGGTT 573

RESULT 8
NTT85A 6053 bp DNA linear PLN 27-FEB-1998
LOCUS N.tobacum T85 gene for auxin-binding protein.
DEFINITION X70902
ACCESSION X70902.1 GI:20033
VERSION X70902.1 GI:20033
KEYWORDS auxin binding protein; T85 gene.
SOURCE Nicotiana tabacum.
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 6053)
REFERENCE Shimomura,S.
AUTHORS Direct Submission Submitted (19-JUN-1993) S. Shimomura, National Institute of
Agrobiological, Resources, Kannondai 2-1-2, Tsukuba, Ibaraki 305,

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[illegible]





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 07:08:40 ; Search time 190 Seconds

(Without alignments)  
5404.796 Million cell updates/sec

Title: US-09-941-042c-1

Perfect score: 456  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1.	456	100.0	456	24	ABL58286
2	456	100.0	1030	18	AAT51750
3	456	100.0	1294	18	AAT51749
4	456	100.0	1372	18	AAT51748
5	456	100.0	1988	18	AAT51747
6	451.2	98.9	2010	18	AAT51746
7	148	32.5	722	18	AAT51751
8	66.6	14.6	5145	24	ABL32348
9	66.6	14.6	5145	24	ABL34464

C	10	66.4	14.6	8305	24	ABL33568	Human immune syste
	11	61	13.4	6175	24	ABL33307	Human immune syste
	12	60.4	13.2	18997	24	ABK33948	Human DNA for stag
	13	60.4	13.2	18997	24	ABL32570	Human immune syste
	14	60.2	13.2	5925	24	ABL33576	Human immune syste
	15	60	13.2	8305	24	ABL33569	Human immune syste
	16	60	13.2	20420	22	AAK73165	Human immune/haema
	17	60	13.2	20420	24	ABK69933	Human secreted pro
	18	59.6	13.1	5407	24	ABL34091	Human immune syste
	19	59.4	13.0	20674	21	AAC58017	Archidonic acid m
	20	59	12.9	494	23	ABV10021	Human prostate exp
	21	58.2	12.8	422	22	AAH15924	Human breast cance
	22	58.2	12.8	700	22	AAH93026	Human inflammatory
	23	58.2	12.8	8842	24	ABL33449	Human immune syste
	24	58.2	12.8	8842	24	AAK63335	Chemically pretrea
	25	58	12.7	6062	24	AAK61094	Human gene regulat
	26	58	12.7	8197	24	ABL70542	Chemically treated
	27	58	12.7	8197	24	ABL34515	Human metastasis a
	28	57.6	12.6	6050	22	AAK46792	Tumour suppressor
	29	57.6	12.6	6050	24	ABK33937	Human DNA for stag
	30	57.6	12.6	6050	24	ABL34129	Human immune syste
	31	57.6	12.6	10279	24	ABL92277	Chemically treated
	32	57.6	12.6	10279	24	ABL33591	Human immune syste
	33	57.6	12.6	10279	24	AAK22328	Chemically treated
	34	57.2	12.5	8085	22	AAK46479	Tumour suppressor
	35	57.2	12.5	8085	24	ABK33986	Human DNA for stag
	36	57	12.5	10886	24	ABL34135	Human immune syste
	37	57	12.5	16258	24	ABL70376	Chemically treated
	38	57	12.5	16258	24	ABK40038	Human chemically p
	39	56.8	12.5	3296	23	ABL17264	Drosophila melanog
	40	56.6	12.4	6013	24	AAK61265	Human gene regulat
	41	56.6	12.4	6013	24	ABK31361	Signal transductio
	42	56.6	12.4	6095	22	AAK46310	Tumour suppressor
	43	56.6	12.4	6095	24	ABL70150	Chemically treated
	44	56.6	12.4	6095	24	ABL32361	Human immune syste
	45	56.6	12.4	6095	24	ABL34475	Human metastasis a

#### ALIGNMENTS

RESULT 1	
ABL58286	
ID ABL58286 standard; DNA; 456 BP.	
AC	ABL58286;
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	N. tabacum N1c gene product responsive element DNA sequence.
XX	
KW	Tobacco; plant; cis-acting element; transgenic; nicotline; N1c;
KW	NCQPI; nitrosamine; responsive element; ds.
XX	
OS	Nicotiana tabacum.
XX	
PN	MO200218607-A2.
XX	
PD	07-MAR-2002.
XX	
PF	28-AUG-2001; 2001WO-US26788.
XX	
PR	30-AUG-2000; 2000US-229198P.
XX	
PA	(UYNC-) UNIV NORTH CAROLINA STATE.
XX	
PI	Conkling MA, LI Y;
XX	
DR	WPI; 2002-371827/40.
XX	
PT	Obtaining plant with altered levels of desired protein regulated
PT	cis-acting element by introducing nucleic acid with the element not
PT	operably linked to coding sequence of the protein to produce a



DT	15-OCT-1997	(first entry)
XX		
DE	Root cortex specific gene TobRD2 promoter (dell.3).	
XX		
KW	Root cortex-specific promoter; TobRD2; tobacco; transgenic plant;	
KM	Insecticide; Bacillus thuringiensis; biological control; ss.	
XX		
OS	Nicotiana tabacum.	
XX		
PN	M09J05261-A1.	
PD		
XX	13-FEB-1997.	
XX		
PF	24-JUL-1996; 96WO-US12158.	
XX		
PR	28-JUL-1995; 95US-0508786.	
XX		
PA	(UNYC-) UNIV NORTH CAROLINA STATE.	
PI	Conkling MA, Mendu N, Song W;	
XX		
DR	WPI: 1997-145698/13.	
XX		
PT	DNA directing heterologous gene expression in the root cortex - used	
PT	e.g. for expressing insecticidal Bacillus proteins	
XX		
PS	Claim 1; Page 36; 53pp; English.	
CC	An isolated DNA (AAT51749), designated dell.3, comprises a 1294 bp	
CC	5'-deletion mutant of the tobacco RD2 gene (TobRD2) promoter (see	
CC	also AAT51745), which directs root cortex-specific expression of	
CC	associated genes. Dell.3 can be used in DNA cassettes to direct	
CC	the expression of heterologous genes in the root cortex layer of	
CC	transgenic monocot or dicot plants, e.g. Bacillus thuringiensis	
CC	crystal proteins in tobacco for the control of root-damaging pests.	
CC	Dell.3 conferred high levels of GUS reporter gene expression	
CC	(several-fold higher than the CamV35S promoter) in transgenic	
CC	tobacco root cortex.	
XX		
SQ	Sequence 1294 BP; 515 A; 174 C; 203 G; 402 T; 0 other;	
	Query Match 100.0%; Score 456; DB 18; Length 1294;	
	Best Local Similarity 100.0%; Pred. No. 4e+68;	
	Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 GGAAACAAATTCACAATCAATGAGTTGGCTACTCATTAATCGTAGAATCTTGCGCCTT	60
DB		
	265 GGAAACAAATTCACAATCAATGAGTTGGCTACTCATTAATCGTAGAATCTTGCGCCTT	324
OY	61 GCATAATAAGAATCTTGGAATAAGCTTAGTTTAAATATAAATAGCATATATGATTTTGA	120
DB		
	325 GCATAATAAGAATCTTGGAATAAGCTTAGTTTAAATATAAATAGCATATATGATTTTGA	384
OY	121 ATTAGTATTGTGAGTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	180
DB		
	385 ATTAGTATTGTGAGTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	444
OY	181 ATGAAAAATTTAAATGCTTATTAATGTTTTAACTTCTATATATAATTTTTCATATGTA	240
DB		
	445 ATGAAAAATTTAAATGCTTATTAATGTTTTAACTTCTATATATAATTTTTCATATGTA	504
OY	241 TTATATCGGTATAGTTCGATATTTTTCATATTTATTTTATATAAAAATTAATTAATTA	300
DB		
	505 TTATATCGGTATAGTTCGATATTTTTCATATTTATTTTATATAAAAATTAATTAATTA	564
OY	301 AATTAATCGGTATAGTTCGATATTTTATATAAAAATCTACGCTTCTCAGAGAACTTAA	360
DB		
	565 AATTAATCGGTATAGTTCGATATTTTATATAAAAATCTACGCTTCTCAGAGAACTTAA	624
OY	361 AATCGGTTCGGGCGGAGCGGTGCATCGGTTTAAAGCATTTTCAAATATTCATGACAC	420
DB		
	625 AATCGGTTCGGGCGGAGCGGTGCATCGGTTTAAAGCATTTTCAAATATTCATGACAC	684

Oy		421 CCTAGTGTGTTATAGCTAAAGAAGCATTACAGAG	456
Dd		     CCTAGTGTGTTATAGCTAAAGAAGCATTACAGAG	720
	RESULT 4		
ID	AAT51748		
XX AC	AAT51748 standard; DNA; 1372 BP.		
XX ATC	AAT51748;		
XX DT	15-OCT-1997 (first entry)		
DE XX	Root cortex specific gene TobRD2 promoter (dell.4).		
RW KM	Root cortex-specific promoter; TobRD2; tobacco; transgenic plant; insecticide; Bacillus thuringiensis; biological control; ss.		
OS XX	Nicotiana tabacum.		
PX PN	M09705261-AI.		
PD XX	13-FEB-1997.		
PE XX	24-JUL-1996; 96MO-US12158.		
PR XX	28-JUL-1995; 95US-0508786.		
PA XX	(UYNCC) UNIV NORTH CAROLINA STATE.		
PI XX	Conkling MA, Mendu N, Song W;		
DR XX	WPI; 1997-145698/13.		
PT PT	DNA directing heterologous gene expression in the root cortex - used e.g. for expressing insecticidal Bacillus proteins		
PS XX	Claim 1; Page 35; 53pp; English.		
CC CC	An isolated DNA (AAT51747), designated dell.4, comprises a 1372 bp 5'-deletion mutant of the tobacco RD2 gene (TobRD2) promoter (see also AAT51746), which directs root cortex-specific expression of associated genes. Dell.4 can be used in DNA cassettes to direct the expression of heterologous genes in the root cortex layer of transgenic monocol or dicot plants, e.g. Bacillus thuringiensis crystal proteins in tobacco for the control of root-damaging pests. Dell.4 conferred high levels of GUS reporter gene expression (several-fold higher than the CaMV35S promoter) in transgenic tobacco root cortex.		
SQ	Sequence 1372 BP; 532 A; 187 C; 215 G; 438 T; 0 other:		
	Query Match            100.0%; Score 456; DB 18; Length 1372; Best Local Similarity 100.0%; Pred. No. 3.9e+68; Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
OY	I GGAAACAATAATTCATCATTTGGTAGTTTTGCCTACTCAATATCGCTAGAAATCTTGACCCT	60	
Dd	       343 GGAAACAATAATTCATCATTTGGTAGTTTTGCCTACTCAATATCGCTAGAAATCTTGACCCT	402	
OY	61 GCATTAATAAGAACCTTGGAATAGCTTAGCTTTAAATTAATAATGCCAAAATAGATTNAGGA	120	
Dd	403 GCTAATTAAGAATCTTGGAATAGCTTAGCTTTAAATTAATAATGCCAAAATAGATTNAGGA	462	
OY	121 ATTAGTATTTTGTAGTTTAATTAATGACTTGTGAACAGTTTTTTAATTCCAAGCCC	180	
Dd	463 ATTAGTATTTTGTAGTTTAATTAATGACTTGTGAACAGTTTTTTAATTCCAAGCCC	522	
OY	181 ATGAAAAATTTAATGCTTTATTTAGTTTAACTACTATATTAATTTTCAAATGTAA	240	
Dd	523 ATGAAAAATTTAATGCTTTATTTAGTTTAACTACTATATTAATTTTCAAATGTAA	582	
OY	241 TTATAATCGGTATAGTTCGATATTTTTCATTTATTTTATAAATAAANAACCTACCT	300	

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Db      583  TTTAATCGGTAATGATGATATTTTTCATTTATTTATATAAAAGCTTACCCT 642
QY      301  AATATCGGTACAGTTATAGATTATATATAAAATCTACGGTCTTCAGAAAGAACTTAA 360
Db      643  AATATCGGTACAGTTATAGATTATATATAAAATCTACGGTCTTCAGAAAGAACTTAA 702
QY      361  AATCGGTTGGTGGGACGGTTCGATCGGTTAGTCGATTTTCAAAATATTCATTGACACT 420
Db      703  AATCGGTTGGTGGGACGGTTCGATCGGTTAGTCGATTTTCAAAATATTCATTGACACT 762
QY      421  CCTAGTGTGTGTATAGTATAAAGCAGTTACAGAG 456
Db      763  CCTAGTGTGTGTATAGTATAAAGCAGTTACAGAG 798

RESULT 5
AAT51747
ID      AAT51747 standard; DNA; 1988 BP.
XX      AAT51747;
XX      AAT51747;
XX      15-OCT-1997 (first entry)
DE      Root cortex specific gene TobRD2 promoter (del2.0).
XX      Root cortex specific promoter; TobRD2; tobacco; transgenic plant;
KW      insecticide; Bacillus thuringiensis; biological control; ss.
XX      Nicotiana tabacum.
XX      MO9705261-A1.
XX      13-FEB-1997.
XX      24-JUL-1996; 96WO-US12158.
XX      28-JUL-1995; 95US-0508786.
XX      (UNNC-) UNIV NORTH CAROLINA STATE.
XX      Conkling MA, Mendu N, Song W;
XX      WPI; 1997-145698/13.
XX      DNA directing heterologous gene expression in the root cortex - used
XX      e.g. for expressing insecticidal Bacillus proteins
XX      Claim 1; Page 33-34; 53pp; English.
XX      An isolated DNA (AAT51747), designated del2.0, comprises a 1988 bp
XX      portion of the tobacco RD2 gene (TobRD2) promoter (see also
XX      AAT51746), which directs root cortex-specific expression of
XX      associated genes. Del2.0 and truncated TobRD2 promoters (see also
XX      AAT51748-56) can be used in DNA cassettes to direct the expression of
XX      heterologous genes in the root cortex layer of transgenic monocot
XX      or dicot plants, e.g. to express Bacillus thuringiensis crystal
XX      proteins in tobacco for the control of root-damaging pests. Del2.0
XX      directed high levels of GUS reporter gene expression (4-fold higher
XX      than the CAM355 promoter) in transgenic tobacco root cortex.
XX      Sequence 1988 BP; 714 A; 271 C; 302 G; 701 T; 0 other;
XX
Query Match      100.0%; Score 456; DB 18; Length 1988;
Best Local Similarity 100.0%; Pred. No. 3,8e-68;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1  GGAACATATTCATATACATTCAGTTGCTACTCATATCCGTGAAATCTTGGCCTT 60
Db      959  GGAACATATTCATATACATTCAGTTGCTACTCATATCCGTGAAATCTTGGCCTT 1018
QY      61  GCTAATAAGTACTGGAATAGCTTAAATATTAATAGCATATACATTTTACGA 120

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Db      1019 GCTAATAAGTACTGGAATAGCTTAAATATTAATAGCATATACATTTTACGA 1078
QY      121  ATTAGATATTTGAGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
Db      1079  ATTAGATATTTGAGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1138
QY      181  ATGAAAAATTTAATGCTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
Db      1139  ATGAAAAATTTAATGCTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1198
QY      241  TTTAATCGGTATTCGATATTTTTCATTTATTTTAAATTAATTAATTAATTAATTAATTAAT 300
Db      1199  TTTAATCGGTATTCGATATTTTTCATTTATTTTAAATTAATTAATTAATTAATTAATTAAT 1258
QY      301  AATATCGGTACAGTTATAGATTATATATAAAATCTACGGTCTTCAGAAAGAACTTAA 360
Db      1259  AATATCGGTACAGTTATAGATTATATATAAAATCTACGGTCTTCAGAAAGAACTTAA 1318
QY      361  AATCGGTTGGTGGGACGGTTCGATCGGTTAGTCGATTTTCAAAATATTCATTGACACT 420
Db      1319  AATCGGTTGGTGGGACGGTTCGATCGGTTAGTCGATTTTCAAAATATTCATTGACACT 1378
QY      421  CCTAGTGTGTGTATAGTATAAAGCAGTTACAGAG 456
Db      1379  CCTAGTGTGTGTATAGTATAAAGCAGTTACAGAG 1414

RESULT 6
AAT51746
ID      AAT51746 standard; DNA; 2010 BP.
XX      AAT51746;
XX      AAT51746;
XX      15-OCT-1997 (first entry)
DE      Root cortex specific gene TobRD2 promoter.
XX      Root cortex specific promoter; TobRD2; tobacco; transgenic plant;
KW      insecticide; Bacillus thuringiensis; biological control; ss.
XX      Nicotiana tabacum.
XX      Key
XX      Location/Qualifiers
XX      TATA_signal
XX      1971..1975
XX      /*tag- a
XX      2000
XX      /*tag- b
XX      /note= "predicted start of transcription"
XX      MO9705261-A1.
XX      13-FEB-1997.
XX      24-JUL-1996; 96WO-US12158.
XX      28-JUL-1995; 95US-0508786.
XX      (UNNC-) UNIV NORTH CAROLINA STATE.
XX      Conkling MA, Mendu N, Song W;
XX      WPI; 1997-145698/13.
XX      DNA directing heterologous gene expression in the root cortex - used
XX      e.g. for expressing insecticidal Bacillus proteins
XX      Claim 1; Page 32-33; 53pp; English.
XX      An isolated DNA (AAT51746) comprises the tobacco RD2 gene (TobRD2)
XX      promoter, which directs root cortex-specific expression of
XX      associated genes. A clone containing the isolated DNA was obtd.
XX      from a tobacco seedling genomic library by screening with TobRD2
XX      cDNA. The antisense strand of TobRD2 was used as a probe to show

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CC that TobRD2 mRNA is expressed only in the cortex layer of roots.  
CC truncations of the promoter region (see also AAT51747-54) were prep.  
CC by PCR. The full-length or truncated promoters can be used in DNA  
CC cassettes to direct root cortex-specific expression of heterologous  
CC genes in transgenic monocot or dicot plants, e.g. to express  
CC Bacillus thuringiensis crystal proteins in tobacco for the control  
CC of root-damaging pests.  
XX  
SQ Sequence 2010 BP; 729 A; 276 C; 303 G; 702 T; 0 other;  
Query Match 98.9%; Score 451.2; DB 18; Length 2010;  
Best Local Similarity 99.3%; Pred. No. 2,4e-67;  
Matches 453; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
YY 1 GGAACATATTCATACATGTAGTTGCTACCATATAGCGATAGTCTGCTT 60  
DB 959 GGAACATATTCATACATGTAGTTGCTACCATATAGCGATAGTCTGCTT 1018  
YY 61 GCTAATAAGATACCTGAAATAGCTTAAATATATATAGCATATAGATTTAGGA 120  
DB 1019 GCTAATAAGATACCTGAAATAGCTTAAATATATATAGCATATAGATTTAGGA 1078  
YY 121 ATTAGTATTTGAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 180  
DB 1079 ATTAGTATTTGAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1138  
YY 181 ATGAAAAATTAATGCTTTTATGTTTAACTACATATTAATTTTCAATNGTAAA 240  
DB 1139 ATGAAAAATTAATGCTTTTATGTTTAACTACATATTAATTTTCAATNGTAAA 1198  
YY 241 TTTATCGGTATGTCGATATTTTCAATTTTATTTTATTTTATTTTATTTTATTTT 300  
DB 1199 TTTATCGGTATGTCGATATTTTCAATTTTATTTTATTTTATTTTATTTTATTTT 1258  
YY 301 AATTAATCGGTACGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360  
DB 1259 AATTAATCGGTACGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1318  
YY 361 AATCGGTTGCGTGGGCGGTTGATGCTTATGATTTTCAATTTTCAATTTGACACT 420  
DB 1319 AATCGGTTGCGTGGGCGGTTGATGCTTATGATTTTCAATTTTCAATTTGACACT 1378  
YY 421 CCTAGTTGTTGTTATAGTAAAAAGCAGTTACAGAG 456  
DB 1379 CCTAGTTGTTGTTATAGTAAAAAGCAGTTACAGAG 1414  
RESULT 7  
AAT51751  
ID AAT51751 standard; DNA: 722 BP.  
XX  
AC AAT51751;  
DT 15-OCT-1997 (first entry)  
XX  
DE Root cortex specific gene TobRD2 promoter (del0.7).  
XX  
KW Root cortex-specific promoter; TobRD2; tobacco; transgenic plant;  
KW Insecticide; Bacillus thuringiensis; biological control; ss.  
XX  
OS Nicotiana tabacum.  
XX  
PN W09705261-A1.  
XX  
PD 13-FEB-1997.  
XX  
PF 24-JUL-1996; 96MO-US12158.  
XX  
PR 28-JUL-1995; 95US-0508786.  
XX  
PA (UTNC-) UNIV NORTH CAROLINA STATE.  
XX  
PI Conkling MA, Mendu N, Song W;

XX  
DR WPI; 1997-145698/13.  
XX  
PT DNA directing heterologous gene expression in the root cortex - used  
PT e.g. for expressing insecticidal Bacillus proteins  
XX  
PS Claim 1; Page 38; 53pp; English.  
XX  
CC An isolated DNA (AAT51751), designated del0.7, comprises a 722 bp  
CC 5'-deletion mutant of the tobacco RD2 gene (TobRD2) promoter (see  
CC also AAT51746), which directs root cortex-specific expression of  
CC associated genes. Del0.7 can be used in DNA cassettes to direct  
CC the expression of heterologous genes in the root cortex layer of  
CC transgenic monocot or dicot plants, e.g. Bacillus thuringiensis  
CC crystal proteins in tobacco for the control of root-damaging pests.  
CC Del0.7 conferred high levels of GUS reporter gene expression  
CC (about twice that of the CamV35 promoter) in transgenic tobacco  
CC root cortex.  
XX  
SQ Sequence 722 BP; 278 A; 107 C; 129 G; 208 T; 0 other;  
Query Match 32.5%; Score 148; DB 18; Length 722;  
Best Local Similarity 100.0%; Pred. No. 1.5e-16;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
YY 309 GTACAGTTATGATTTATATATATATATATATATATATATATATATATATATAT 368  
DB 1 GTACAGTTATGATTTAT 60  
YY 369 CGGTGCGGAGCGGTTCGATGCGTTTATGATTTTCAATATATATATATATATATAT 428  
DB 61 CGGTGCGGAGCGGTTCGATGCGTTTATGATTTTCAATATATATATATATATATATAT 120  
YY 429 TTGTTATAGTAAAAAGCAGTTACAGAG 456  
DB 121 TTGTTATAGTAAAAAGCAGTTACAGAG 148  
RESULT 8  
ABL32348  
ID ABL32348 standard; DNA: 5145 BP.  
XX  
AC ABL32348;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Human immune system associated gene SEQ ID NO: 321.  
XX  
KW Human; immune system disease; cytosine methylation; antileukemic;  
KW antileukemic; antileukemic; cytostatic; neutropenic;  
KW neutropenic; anti-HIV; anticonvulsant; ophthalmologic;  
KW antineoplastic; antineoplastic; antidiabetic; antiparasitic;  
KW antineoplastic; cancer; eye disease; arteriosclerosis; anemia;  
KW acute myeloid leukemia; Alzheimer's disease; AIDS; epilepsy;  
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
KW gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN W0200200928-A2.  
XX  
PD 03-JAN-2002.  
XX  
PF 02-JUL-2001; 2001WO-EP07537.  
XX  
PR 30-JUN-2000; 2000DE-1032529.  
XX  
PR 01-SEP-2000; 2000DE-1043826.  
XX  
PA (EPIC-) EPICOMICS AG.  
XX  
PI Olek A, Plepenbrock C, Berlin K;  
XX  
DR WPI; 2002-130909/17.



PF 02-JUL-2001; 2001WO-EP07537.  
XX  
XX 30-JUN-2000; 2000DE-1032529.  
PR 01-SEP-2000; 2000DE-1043826.  
XX  
XX (EPIC-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2002-130909/17.  
XX  
XX Nucleic acid comprising fragment of chemically modified gene, useful  
PT for diagnosis and treatment of diseases associated with abnormal  
PT cytosine methylation -  
XX  
XX Claim 1; SEQ ID NO 1541; 32pp + Sequence Listing; German.  
XX  
XX The present invention provides a number of human immune system associated  
CC genes which are modified by the methylation of cytosines. The sequences  
CC can be used in the diagnosis and treatment of immune system disorders,  
CC including eye diseases such as retinopathy, neovascular glaucoma and  
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
CC rheumatoid arthritis, psoriasis and inflammatory/intestinal bowel  
CC diseases. The present sequence is a gene of the invention.  
XX  
SQ Sequence 8305 BP; 2181 A; 185 C; 1901 G; 4038 T; 0 other;  
Query Match 14.6%; Score 66.4; DB 24; Length 8305;  
Best Local Similarity 49.2%; Pred. No. 0.0056;  
Matches 175; Conservative 0; Mismatches 181; Indels 0; Gaps 0;  
QY 8 TATTCAATCACTGAGTTGGTCTACTCAATACGCTAGAACTTTGGCCCTGCTAATA 67  
DB 6424 TATTATATATATAATAATAATAATAATAATAATAATAATAATAATAATAATA 6365  
QY 68 AAGATCACTGAAATGCTAGTTTAAATATAATAATAATAATAATAATAATAATAATA 127  
DB 6364 AAAATATATATTTATATATATTTCAATTTATATATATATATATATATATATATA 6305  
QY 128 TTTTGAGTTTAATTTCTTATTTGACCTGTAAAGTTTAAATTTCCAAAGCCCAAGAAA 187  
DB 6304 TAAATATATATATAATAATAATAATAATAATAATAATAATAATAATAATAATA 6245  
QY 188 ATTAAATGCTTTATAGTTTAACTTACTATATATATATTTTCAATATGTAATTAATC 247  
DB 6244 AATA 6185  
QY 248 GGTATAGTTCGATATTTTTCATTTTATTTTAAATAATAATAATAATAATAATAATC 307  
DB 6184 TAAATA 6125  
QY 308 GGTACAGTTATAGATTATATAATAATAATAATAATAATAATAATAATAATAATAAT 363  
DB 6124 TATATATTTTAT 6069  
RESULT 11  
ABL33307  
ID ABL33307 standard; DNA; 6175 BP.  
XX  
XX ABL33307;  
XX  
XX 26-MAR-2002 (first entry)  
XX  
XX Human immune system associated gene SEQ ID NO: 1280.  
XX  
XX Human; immune system disease; cytosine methylation; antiasthmatic;  
KW antiarteriosclerotic; antihaemtic; cytosinetic; nootropic;  
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
KW antineumatic; antiarthritic; antidiabetic; antipsoriatic;  
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;

KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
KW gene; ds.  
XX  
XX Homo sapiens.  
OS  
XX WO200200928-A2.  
XX  
XX  
XX 03-JAN-2002.  
XX  
XX  
XX 02-JUL-2001; 2001WO-EP07537.  
XX  
XX 30-JUN-2000; 2000DE-1032529.  
PR 01-SEP-2000; 2000DE-1043826.  
XX  
XX (EPIC-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2002-130909/17.  
XX  
XX Nucleic acid comprising fragment of chemically modified gene, useful  
PT for diagnosis and treatment of diseases associated with abnormal  
PT cytosine methylation -  
XX  
XX Claim 1; SEQ ID NO 1280; 32pp + Sequence Listing; German.  
XX  
XX The present invention provides a number of human immune system associated  
CC genes which are modified by the methylation of cytosines. The sequences  
CC can be used in the diagnosis and treatment of immune system disorders,  
CC including eye diseases such as retinopathy, neovascular glaucoma and  
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
CC rheumatoid arthritis, psoriasis and inflammatory/intestinal bowel  
CC diseases. The present sequence is a gene of the invention.  
XX  
SQ Sequence 6175 BP; 1506 A; 154 C; 1357 G; 3158 T; 0 other;  
Query Match 13.4%; Score 61; DB 24; Length 6175;  
Best Local Similarity 48.7%; Pred. No. 0.046;  
Matches 166; Conservative 0; Mismatches 175; Indels 0; Gaps 0;  
QY 7 AATTCATATCACTGAGTTGCTACTCATTAATCGCTAGAACTTTGGCTGCTAAT 66  
DB 4615 AATTTATTTATTTGTAATTTATATATATATATATATATATATATATATATATAT 4674  
QY 67 AAAGATCTTGAATAGCTTACTTAAATATATATATATATATATATATATATATATAT 126  
DB 4675 AATTTA 4734  
QY 127 ATTTGAGTTTAAATCTATATGACTGTAAAGTTTAAATAATCCAAAGCCCAAGAAA 186  
DB 4735 TGTTTTATATATATGTTATATATATATATATATATATATATATATATATATATAT 4794  
QY 187 AATTTAAATGCTTATATAGTTTAACTTAACTTAAATAATAATAATAATAATAATAAT 246  
DB 4795 GTTTAAATTTAT 4854  
QY 247 CGGTATAGTTCATATTTTTCATATTTTAAATAATAATAATAATAATAATAATAAT 306  
DB 4855 AATTTATTTTATGTTTATATATTTTATATATATATATATATATATATATATATAT 4914  
QY 307 CGGTACAGTTATAGATTATATAATAATAATAATAATAATAATAATAATAATAAT 347  
DB 4915 GTATTTATTTAT 4955  
RESULT 12  
ABK33948  
ID ABK33948 standard; DNA; 18997 BP.  
XX  
XX ABK33948;  
XX  
XX 18-JUN-2002 (first entry)

DE Human DNA for staging of Astrocytomas #16.  
 XX Human: ds; astrocytoma; cytosatic; staging; cysteine methylation; Cpg;  
 KM bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry;  
 KM matrix assisted laser desorption/ionization mass spectrometry.  
 XX Homo sapiens.  
 OS WO200202808-AZ.  
 PN 10-JAN-2002.  
 PD 02-JUL-2001; 2001WO-EP07538.  
 PF 30-JUN-2000; 2000DE-1033529.  
 PR 01-SEP-2000; 2000DE-1043826.  
 XX (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Plepenbrock C, Berlin K;  
 PI WPI: 2002-171649/22.  
 DR Novel chemically modified genomic DNA sequences, useful in the  
 XX characterisation, classification, differentiation, grading, staging,  
 PT treatment and/or diagnosis of astrocytomas or predisposition to  
 PT astrocytomas -  
 XX  
 PS Claim 1: SEQ ID NO 31: 37pp: English.  
 CC The invention relates to a nucleic acid comprising a sequence (I) of at  
 CC least 18 bases in length of a segment of chemically pre-treated genomic  
 CC DNA which has any one of the sequences of (ABK33919-ABK34032) or its  
 CC complement. Also included are an oligonucleotide or peptide nucleic  
 CC acid (or set thereof) of at least 9 nucleotides which hybridises to (I),  
 CC primers for (I), probes for detecting cytosine methylation or single-  
 CC nucleotide polymorphisms (SNP) in (I), an array of oligomers  
 CC or peptide nucleic acids for analysing diseases associated with the  
 CC methylation states of the Cpg dinucleotides of (I). The array is useful  
 CC for determining genetic and/or epigenetic parameters, classification,  
 CC differentiation, grading, staging, treatment and/or diagnosis of  
 CC astrocytomas, or the predisposition to astrocytomas by analysing cytosine  
 CC methylations, involves obtaining a biological sample containing genomic  
 CC DNA, extracting the genomic DNA, converting cytosine bases which are  
 CC unethylated at the 5-position, in the genomic DNA sample, to uracil or  
 CC another base which is dissimilar to cytosine in terms of hybridisation  
 CC behaviour, by chemical treatment and amplifying chemically pre-treated  
 CC genomic DNA fragments using the array and a polymerase, where the  
 CC amplification carries a detectable label. The method further involves  
 CC identifying methylation status of one or more cytosine positions, and  
 CC analysing methylation status of the cytosine positions by reference to  
 CC one or more data sets. The genomic DNA is chemically treated by using a  
 CC bisulphite, hydrogen sulphite or disulphite. The amplification  
 CC step amplifies DNA which is of particular interest in astrocytoma or  
 CC brain tissue, based on the specific genomic methylation status of brain  
 CC tissues, as opposed to background DNA. The amplification carries a  
 CC fluorescent label or radiolabel. Optionally, the labels of the  
 CC amplification are detachable molecule fragments having a typical mass  
 CC which are detected in a mass spectrometer. The fragments of chemically  
 CC pre-treated genomic DNA to be amplified, have a single positive or  
 CC negative charge for a better detectability in the mass spectrometer.  
 CC Preferably, the amplification or fragments of the amplification are  
 CC detected by matrix assisted laser desorption/ionisation mass spectrometry  
 CC (MALDI) or using electron spray mass spectrometry (ESI). The  
 CC present sequence is one of the chemically pre-treated reference DNA  
 CC samples of the invention.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 CC Sequence 18997 BP: 4675 A: 299 C: 4016 G: 10007 T: 0 other:

Query Match 13.2%; Score 60.4; DB 24; Length 18997;  
 Best Local Similarity 49.7%; Pred. No. 0.053;  
 Matches 154; Conservative 0; Mismatches 156; Indels 0; Gaps 0;  
 OY 19 TTGATGTTGGCTACTCAATATCGCTAGAAATCTTGTGCTGCTTAATGAATCTTGA 78  
 DB 13515 TTGAGCTTTTATTTTATTTGCGGATTTTGTATATATTTTATTTGAATAATTTGG 13574  
 OY 79 AATAGCTTAGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 138  
 DB 13575 TTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 13634  
 OY 139 ATTACTTATGACCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 198  
 DB 13635 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 13694  
 OY 199 TATTAGTTTAACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 258  
 DB 13695 TATTATTAATGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTA 13754  
 OY 259 ATATTTTTCATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 318  
 DB 13755 ATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 13814  
 OY 319 AGATTATAT 328  
 DB 13815 GATTTCGTTT 13824  
 RESULT 13  
 ABL32570  
 ID ABL32570 standard: DNA; 18997 BP.  
 XX  
 AC ABL32570:  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Human immune system associated gene SEQ ID NO: 543.  
 XX  
 KM Human; immune system disease; cytosine methylation; antiasthmatic;  
 KM antiarteriosclerotic; antiandemic; cytosatic; noctropic;  
 KM neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
 KM antirheumatic; antiarthritic; antidiabetic; antipsoriatic;  
 KM antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
 KM acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
 KM neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
 KM gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200928-AZ.  
 XX  
 PD 03-JAN-2002.  
 PF 02-JUL-2001; 2001WO-EP07537.  
 PR 30-JUN-2000; 2000DE-1033529.  
 PR 01-SEP-2000; 2000DE-1043826.  
 XX (EPIG-) EPIGENOMICS AG.  
 PA Olek A, Plepenbrock C, Berlin K;  
 PI WPI: 2002-130909/17.  
 DR Novel chemically modified genomic DNA sequences, useful in the  
 XX characterisation, classification, differentiation, grading, staging,  
 PT treatment and/or diagnosis of diseases associated with abnormal  
 PT cytosine methylation -  
 XX  
 PS Claim 1: SEQ ID NO 543: 32pp + Sequence Listing; German.  
 CC The present invention provides a number of human immune system associated



XX (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2002-130909/17.

PT Nucleic acid comprising fragment of chemically modified gene, useful  
PT for diagnosis and treatment of diseases associated with abnormal  
PT cytosine methylation -

PS Claim 1; SEQ ID NO 1542; 32pp + Sequence Listing; German  
vz

CC The present invention provides a number of human immune system associated  
CC genes which are modified by the methylation of cytosines. The sequences  
CC can be used in the diagnosis and treatment of immune system disorders,  
CC including eye diseases such as retinopathy, neovascular glaucoma and  
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
CC rheumatoid arthritis, psoriasis and inflammatory/allergic bowel  
CC diseases. The present sequence is a gene of the invention.

**SQ** Sequence 8305 BP; 2163 A; 185 C; 2060 G; 3897 T; 0 other;

Query Match:	13.2%	Score 60;	DB 24;	Length 8305;
Best Local Similarity:	48.0%	Pred. No.	0.066;	
Matches 171;	Conservative	0;	Mismatches 185;	Indels 0;
			Gaps	0

8 TATTCATACATTGTAGTTTGCTACTCATATCGCTAGATACTTTGTGCCTGCTATA 67

Db 1882 TATTTATTATATAATATATGTTATAAATATATATAATTTAATATATATTTATTTA 1941

68 AACGATCTTGAATAGCTTAGTTAAATATAAATAGCATAATAGATTTTAGGAATTAGTA 127

Db 1942 AGAATATATTATTATATATTATAATTAAATATATATATATATATATAA 2001

128 TTTGAGTTTAATTACTTATTGACTTGTAACAGTTTTTTATAATTCCAAGGCCCATGAAA 187

**Dd**      2002 TAATATATATAATATATATATTATTAATAAATATATATATAT 2061

188 ATTTCAGCTTATAGTTTAACTTACTATATAAATTTCATATGTAANAATTATC 247

[illegible]

248 GGTAATGTCGATAATTTTTCATTTATTTTAAATAAAAACTTACCCCTAATTAAC 30/

[illegible]

27 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1

[illegible]

Search completed: June 9, 2003, 07:16:39  
Job time : 192 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 07:13:20 ; Search time 44 Seconds  
(without alignments)  
3178.286 Million cell updates/sec

Title: US-09-941-042C-1

Perfect score: 456  
Sequence: 1 ggaacatattcaatcatl.....gttaaaagcagttacagag 456

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq: \*  
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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	456	100.0	1030	2	US-08-508-786-5	Sequence 5, Appl1
2	456	100.0	1030	5	PCT-US96-12158-5	Sequence 5, Appl1
3	456	100.0	1294	2	US-08-508-786-4	Sequence 4, Appl1
4	456	100.0	1294	5	PCT-US96-12158-4	Sequence 4, Appl1
5	456	100.0	1372	2	US-08-508-786-3	Sequence 3, Appl1
6	456	100.0	1372	5	PCT-US96-12158-3	Sequence 3, Appl1
7	456	100.0	1988	2	US-08-508-786-2	Sequence 2, Appl1
8	456	100.0	1988	5	PCT-US96-12158-2	Sequence 2, Appl1
9	456	100.0	2010	2	US-08-508-786-1	Sequence 1, Appl1
10	456	100.0	2010	5	PCT-US96-12158-1	Sequence 1, Appl1
11	148	32.5	722	2	US-08-508-786-6	Sequence 6, Appl1
12	148	32.5	722	5	PCT-US96-12158-6	Sequence 6, Appl1
13	60.6	13.3	837	4	US-08-998-416-288	Sequence 288, App
14	59.4	13.0	20674	4	US-09-641-638-651	Sequence 651, App
15	55.6	12.2	636	4	US-08-998-416-1137	Sequence 1137, App
16	52.8	11.6	615	4	US-08-998-416-1186	Sequence 186, App
17	52.8	11.6	1850	3	US-08-617-860B-32	Sequence 32, Appl
18	52.8	11.6	4098	2	US-08-605-106-4	Sequence 4, Appl
19	52.6	11.5	319	1	US-07-593-657-14	Sequence 14, Appl
20	52.6	11.5	1241	1	US-07-593-657-6	Sequence 6, Appl1
21	52.6	11.5	1241	4	US-08-942-012B-3	Sequence 3, Appl1
22	51.4	11.3	665	2	US-08-883-795A-36	Sequence 36, Appl
23	51.4	11.3	3618	1	US-07-872-678A-36	Sequence 36, Appl
24	51.4	11.3	724	4	US-08-998-416-683	Sequence 683, App
25	50.8	11.1	665	2	US-08-883-795A-36	Sequence 36, Appl
26	49.8	10.9	6243	2	US-09-056-075-1	Sequence 1, Appl1
27	49.2	10.8	5108	4	US-09-306-446C-8	Sequence 8, Appl1

28	48.6	10.7	5852	1	US-07-867-106-2	Sequence 2, Appl1
29	48.6	10.7	8920	2	US-08-446-855A-1	Sequence 1, Appl1
30	48.6	10.7	8920	4	US-09-150-741-1	Sequence 1, Appl1
31	48.4	10.6	19124	4	US-08-487-826B-13	Sequence 13, Appl
32	48.4	10.6	20674	4	US-09-641-638-651	Sequence 651, App
33	47.8	10.5	854	4	US-08-998-416-534	Sequence 534, App
34	47.8	10.5	860	4	US-08-998-416-287	Sequence 287, App
35	47.8	10.5	6124	4	US-08-213-419B-3	Sequence 3, Appl1
36	47.4	10.4	663	4	US-08-998-416-191	Sequence 191, App
37	47.4	10.4	19124	2	US-08-487-826B-13	Sequence 13, Appl
38	47.2	10.4	615	4	US-08-998-416-186	Sequence 186, App
39	47.2	10.4	51952	3	US-08-947-823-1	Sequence 1, Appl1
40	47	10.3	8920	2	US-08-446-855A-1	Sequence 1, Appl1
41	47	10.3	8920	4	US-09-150-741-1	Sequence 1, Appl1
42	46.8	10.3	162450	4	US-09-345-882-1	Sequence 13, Appl
43	46.6	10.2	7521	4	US-09-004-838-116	Sequence 116, App
44	46.4	10.2	636	4	US-08-998-416-1137	Sequence 1137, App
45	46.4	10.2	837	4	US-08-998-416-288	Sequence 288, App

#### ALIGNMENTS

RESULT 1  
US-08-508-786-5  
Sequence 5, Application US/08508786  
Patent No. 5837876  
GENERAL INFORMATION:  
APPLICANT: Conkling, Mark A.  
APPLICANT: Mendu, Nandini  
TITLE OF INVENTION: Root Cortex Specific Gene Promoter  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenneth D. Sidley, Bell, Seltzer, Park &  
ADDRESS: Gibson  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: No. 5837876th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/508, 786  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sidley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5051-294  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-420-2200  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1030 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-508-786-5  
Query Match 100.0%; Score 456; DB 2; Length 1030;  
Best local similarity 100.0%; Pred. No. 5.5e-85;  
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGAACATATTCAATCATATGTAAGTCTGCTACTACATATCGCTGAAATACCTTGTGCTT 60  
DB 1 GGAACATATTCAATCATATGTAAGTCTGCTACTACATATCGCTGAAATACCTTGTGCTT 60

QY 61 GCTAATAAGACTGTAAGTACTGTTAATATATATAGCATATAGATTGTTAGCA 120  
 DB 61 GCTAATAAGACTGTAAGTACTGTTAATATATATAGCATATAGATTGTTAGCA 120  
 QY 121 ATTACTATTTGAGTTTATTTACTTATGACTGTGAAGCTTTTATATATCCAGGCC 180  
 DB 121 ATTACTATTTGAGTTTATTTACTTATGACTGTGAAGCTTTTATATATCCAGGCC 180  
 QY 181 ATGAAAAATTATATCTTATATAGTTTAACTACTATATATATATTTTCAATATGATA 240  
 DB 181 ATGAAAAATTATATCTTATATAGTTTAACTACTATATATATATTTTCAATATGATA 240  
 QY 241 TTTAATCGGTATAGTTCATATTTTCAATATTTTATATATATATATATATATATAT 300  
 DB 241 TTTAATCGGTATAGTTCATATTTTCAATATTTTATATATATATATATATATATAT 300  
 QY 301 AATTATCGGTACAGTTATAGTATATATATATATATATATATATATATATATATATAT 360  
 DB 301 AATTATCGGTACAGTTATAGTATATATATATATATATATATATATATATATATATAT 360  
 QY 361 AATCGGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 420  
 DB 361 AATCGGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 420  
 QY 421 CCTAGTTTGTGTATAGTATATATATATATATATATATATATATATATATATATAT 456  
 DB 421 CCTAGTTTGTGTATAGTATATATATATATATATATATATATATATATATATATAT 456

RESULT 2

PCT-US96-12158-5  
 ; Sequence 5, Application PCT/US9612158  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Konkling, Mark A.  
 ; APPLICANT: Mendu, Nandini  
 ; APPLICANT: Song, Men  
 ; TITLE OF INVENTION: Root Cortex Specific Gene Promoter  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kenneth D. Sibley, Bell, Seltzer, Park &  
 ; STREET: Post Office Drawer 34009  
 ; CITY: Charlotte  
 ; STATE: North Carolina  
 ; COUNTRY: USA  
 ; ZIP: 28234  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US96/12158  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sibley, Kenneth D.  
 ; REGISTRATION NUMBER: 31,665  
 ; REFERENCE/DOCKET NUMBER: 5051-294  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 919-420-2200  
 ; TELEFAX: 919-881-3175  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1030 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; PCT-US96-12158-5

Query Match 100.0%; Score 456; DB 5; Length 1030;

Best Local Similarity 100.0%; Pred. No. 5.5e-85;  
 Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGAACATATTCATACATATTTGAGTTTGGTACTCATATTCGCTAATATACCTTGCCCT 60  
 DB 1 GGAACATATTCATACATATTTGAGTTTGGTACTCATATTCGCTAATATACCTTGCCCT 60  
 QY 61 GCTAATAAGACTGTAAGTACTGTTAATATATATATATATATATATATATATATATAT 120  
 DB 61 GCTAATAAGACTGTAAGTACTGTTAATATATATATATATATATATATATATATATAT 120  
 QY 121 ATTACTATTTGAGTTTATTTACTTATGACTGTGAAGCTTTTATATATCCAGGCC 180  
 DB 121 ATTACTATTTGAGTTTATTTACTTATGACTGTGAAGCTTTTATATATCCAGGCC 180  
 QY 181 ATGAAAAATTATATCTTATATAGTTTAACTACTATATATATATATATATATATATATAT 240  
 DB 181 ATGAAAAATTATATCTTATATAGTTTAACTACTATATATATATATATATATATATATAT 240  
 QY 241 TTTAATCGGTATAGTTCATATTTTCAATATTTTATATATATATATATATATATATATAT 300  
 DB 241 TTTAATCGGTATAGTTCATATTTTCAATATTTTATATATATATATATATATATATATAT 300  
 QY 301 AATTATCGGTACAGTTATAGTATATATATATATATATATATATATATATATATATATAT 360  
 DB 301 AATTATCGGTACAGTTATAGTATATATATATATATATATATATATATATATATATATAT 360  
 QY 361 AATCGGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 420  
 DB 361 AATCGGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 420  
 QY 421 CCTAGTTTGTGTATAGTAT 456  
 DB 421 CCTAGTTTGTGTATAGTAT 456

RESULT 3

US-08-508-786-4  
 ; Sequence 4, Application US/08508786  
 ; Patent No. 5837876  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Konkling, Mark A.  
 ; APPLICANT: Mendu, Nandini  
 ; APPLICANT: Song, Men  
 ; TITLE OF INVENTION: Root Cortex Specific Gene Promoter  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kenneth D. Sibley, Bell, Seltzer, Park &  
 ; STREET: Post Office Drawer 34009  
 ; CITY: Charlotte  
 ; STATE: No. 5837876h Carolina  
 ; COUNTRY: USA  
 ; ZIP: 28234  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/508,786  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sibley, Kenneth D.  
 ; REGISTRATION NUMBER: 31,665  
 ; REFERENCE/DOCKET NUMBER: 5051-294  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 919-420-2200  
 ; TELEFAX: 919-881-3175  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1294 base pairs





APPLICATION NUMBER: US/08/508,786  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5051-294  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-420-2200  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1372 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-508-786-3

Query Match 100.0%; Score 456; DB 2; Length 1372;  
Best Local Similarity 100.0%; Pred. No. 5,66-85;

Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAACATATTCATACATTTGCTGCTCTCTATTCGCTGAGATCTTTGCTCT 60  
DB 343 GGAACATATTCATACATTTGCTGCTCTCTATTCGCTGAGATCTTTGCTCT 402  
QY 61 GCTATAAAGATCTGTAATAGCTTATTAATAAATAGCATATAGATTTAGGA 120  
DB 403 GCTATAAAGATCTGTAATAGCTTATTAATAAATAGCATATAGATTTAGGA 462  
QY 121 ATAGATATTTGAGTTATTAATCTTATGACTTGTACAGTTTATTAATCCAGGCC 180  
DB 463 ATAGATATTTGAGTTATTAATCTTATGACTTGTACAGTTTATTAATCCAGGCC 522  
QY 181 ATGAAAAATTAAGCTTATTAATCTTATGACTTGTACAGTTTATTAATCCAGGCC 240  
DB 523 ATGAAAAATTAAGCTTATTAATCTTATGACTTGTACAGTTTATTAATCCAGGCC 582  
QY 241 TTTAATCGGTATGATGCTATTTTTCATTTTATTAATAAATAGCTTACCT 300  
DB 583 TTTAATCGGTATGATGCTATTTTTCATTTTATTAATAAATAGCTTACCT 642  
QY 301 AATTATCGGTACAGTTATAGATTTATTAATAAATCTAGCTTCTCAGAGAACTTAA 360  
DB 643 AATTATCGGTACAGTTATAGATTTATTAATAAATCTAGCTTCTCAGAGAACTTAA 702  
QY 361 AATCGGTTCGCTGGGAGCGTTCATCGCTTATGCTGATTTCAATATTTGACACT 420  
DB 703 AATCGGTTCGCTGGGAGCGTTCATCGCTTATGCTGATTTCAATATTTGACACT 762  
QY 421 CCTAGTGTGTTATAGGTAATAAAGCAGTTACAGAG 456  
DB 763 CCTAGTGTGTTATAGGTAATAAAGCAGTTACAGAG 798

RESULT 6  
PCT-US96-12158-3

Sequence 3, Application PC/TUS9612158  
GENERAL INFORMATION:

APPLICANT: Conkling, Mark A.  
APPLICANT: Mendu, Nandini

APPLICANT: Song, Wen  
TITLE OF INVENTION: Root Cortex Specific Gene Promoter

NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenneth D. Sibley, Bell, Seltzer, Park &  
ADDRESS: Gibson

STREET: Post Office Drawer 34009  
CITY: Charlotte

STATE: North Carolina  
COUNTRY: USA

ZIP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12158

FILING DATE:  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.

REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5051-294

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-420-2200

TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1372 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

PCT-US96-12158-3

Query Match 100.0%; Score 456; DB 5; Length 1372;  
Best Local Similarity 100.0%; Pred. No. 5,66-85;

Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAACATATTCATACATTTGCTGCTCTCTATTCGCTGAGATCTTTGCTCT 60  
DB 343 GGAACATATTCATACATTTGCTGCTCTCTATTCGCTGAGATCTTTGCTCT 402  
QY 61 GCTATAAAGATCTGTAATAGCTTATTAATAAATAGCATATAGATTTAGGA 120  
DB 403 GCTATAAAGATCTGTAATAGCTTATTAATAAATAGCATATAGATTTAGGA 462  
QY 121 ATAGATATTTGAGTTATTAATCTTATGACTTGTACAGTTTATTAATCCAGGCC 180  
DB 463 ATAGATATTTGAGTTATTAATCTTATGACTTGTACAGTTTATTAATCCAGGCC 522  
QY 181 ATGAAAAATTAAGCTTATTAATCTTATGACTTGTACAGTTTATTAATCCAGGCC 240  
DB 523 ATGAAAAATTAAGCTTATTAATCTTATGACTTGTACAGTTTATTAATCCAGGCC 582  
QY 241 TTTAATCGGTATGATGCTATTTTTCATTTTATTAATAAATAGCTTACCT 300  
DB 583 TTTAATCGGTATGATGCTATTTTTCATTTTATTAATAAATAGCTTACCT 642  
QY 301 AATTATCGGTACAGTTATAGATTTATTAATAAATCTAGCTTCTCAGAGAACTTAA 360  
DB 643 AATTATCGGTACAGTTATAGATTTATTAATAAATCTAGCTTCTCAGAGAACTTAA 702  
QY 361 AATCGGTTCGCTGGGAGCGTTCATCGCTTATGCTGATTTCAATATTTGACACT 420  
DB 703 AATCGGTTCGCTGGGAGCGTTCATCGCTTATGCTGATTTCAATATTTGACACT 762  
QY 421 CCTAGTGTGTTATAGGTAATAAAGCAGTTACAGAG 456  
DB 763 CCTAGTGTGTTATAGGTAATAAAGCAGTTACAGAG 798

RESULT 7  
US-08-508-786-2

Sequence 2, Application US/08508786  
Patent No. 5837876

GENERAL INFORMATION:  
APPLICANT: Conkling, Mark A.

APPLICANT: Mendu, Nandini  
APPLICANT: Song, Wen

TITLE OF INVENTION: Root Cortex Specific Gene Promoter  
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenneth D. Sibley, Bell, Seltzer, Park &  
ADDRESSEE: Gibson  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: No. 5837876th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/508,786  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5051-294  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-420-2200  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1988 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-508-786-2

Query Match 100.0%; Score 456; DB 2; Length 1988;

Best Local Similarity 100.0%; Pred. No. 5.8e-85;

Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAACATATTCATACATGTAGTTGCTACTCATATGCTAGATAGTCTTGCTT 60  
DB 959 GGAACATATTCATACATGTAGTTGCTACTCATATGCTAGATAGTCTTGCTT 1018  
QY 61 GCTAATTAAGATCTGGAATAGCTTAAATTAATTAATTAATTAATTAATTA 120  
DB 1019 GCTAATTAAGATCTGGAATAGCTTAAATTAATTAATTAATTAATTAATTA 1078  
QY 121 ATTAGATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 180  
DB 1079 ATTAGATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1138  
QY 181 ATGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240  
DB 1139 ATGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1198  
QY 241 TTTAATCGGATAGTTCGATATTTTCAATTTTAAATTAATTAATTAATTAATTA 300  
DB 1199 TTTAATCGGATAGTTCGATATTTTCAATTTTAAATTAATTAATTAATTAATTA 1258  
QY 301 AATTATCGGATAGTTCGATATTTTCAATTTTAAATTAATTAATTAATTAATTA 360  
DB 1259 AATTATCGGATAGTTCGATATTTTCAATTTTAAATTAATTAATTAATTAATTA 1318  
QY 361 AATCGGATAGTTCGATATTTTCAATTTTAAATTAATTAATTAATTAATTAATTA 420  
DB 1319 AATCGGATAGTTCGATATTTTCAATTTTAAATTAATTAATTAATTAATTAATTA 1378  
QY 421 CCTAGTTGTTGTTATAGTAAAAAGCAGTTACAGAG 456  
DB 1379 CCTAGTTGTTGTTATAGTAAAAAGCAGTTACAGAG 1414

RESULT 8  
PCT-US96-12158-2  
Sequence 2, Application PC/TUS9612158  
GENERAL INFORMATION:

APPLICANT: Conkling, Mark A.  
APPLICANT: Mendu, Nandini  
APPLICANT: Song, Wen  
TITLE OF INVENTION: Root Cortex Specific Gene Promoter  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenneth D. Sibley, Bell, Seltzer, Park &  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: North Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12158  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5051-294  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-420-2200  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1988 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US96-12158-2

Query Match 100.0%; Score 456; DB 5; Length 1988;

Best Local Similarity 100.0%; Pred. No. 5.8e-85;

Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAACATATTCATACATGTAGTTGCTACTCATATGCTAGATAGTCTTGCTT 60  
DB 959 GGAACATATTCATACATGTAGTTGCTACTCATATGCTAGATAGTCTTGCTT 1018  
QY 61 GCTAATTAAGATCTGGAATAGCTTAAATTAATTAATTAATTAATTAATTA 120  
DB 1019 GCTAATTAAGATCTGGAATAGCTTAAATTAATTAATTAATTAATTAATTA 1078  
QY 121 ATTAGATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 180  
DB 1079 ATTAGATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1138  
QY 181 ATGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240  
DB 1139 ATGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1198  
QY 241 TTTAATCGGATAGTTCGATATTTTCAATTTTAAATTAATTAATTAATTAATTA 300  
DB 1199 TTTAATCGGATAGTTCGATATTTTCAATTTTAAATTAATTAATTAATTAATTA 1258  
QY 301 AATTATCGGATAGTTCGATATTTTCAATTTTAAATTAATTAATTAATTAATTA 360  
DB 1259 AATTATCGGATAGTTCGATATTTTCAATTTTAAATTAATTAATTAATTAATTA 1318  
QY 361 AATCGGATAGTTCGATATTTTCAATTTTAAATTAATTAATTAATTAATTAATTA 420  
DB 1319 AATCGGATAGTTCGATATTTTCAATTTTAAATTAATTAATTAATTAATTAATTA 1378  
QY 421 CCTAGTTGTTGTTATAGTAAAAAGCAGTTACAGAG 456  
DB 1379 CCTAGTTGTTGTTATAGTAAAAAGCAGTTACAGAG 1414

## RESULT 9

US-08-508-786-1

Sequence 1, Application US/08508786  
Patent No. 5837876

GENERAL INFORMATION:

APPLICANT: Conkling, Mark A.

APPLICANT: Mendu, Nandini

APPLICANT: Song, Wen

TITLE OF INVENTION: Root Cortex Specific Gene Promoter

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenneth D. Sibley, Bell, Seltzer, Park &amp;

ADDRESS: Gldson

STREET: Post Office Drawer 34009

CITY: Charlotte

STATE: No. 5837876th Carolina

COUNTRY: USA

ZIP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/508.786

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Sibley, Kenneth D.

REGISTRATION NUMBER: 31,665

REFERENCE/DOCKET NUMBER: 5051-294

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-420-2200

TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2010 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-508-786-1

Query Match

Best Local Similarity 100.0%; Score 456; DB 2; Length 2010;

Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GGAACATATTCATACATCTGCTACTGCTATATCGCTAGAACTTTGCTT 60  
1139 GGAACATATTCATACATCTGCTACTGCTATATCGCTAGAACTTTGCTT 1018  
Db 61 GCTAATAAGTACTGTAATAGCTTAAATATTAATAGCATATAGATTTAGA 120  
1019 GCTAATAAGTACTGTAATAGCTTAAATATTAATAGCATATAGATTTAGA 1078  
Db 121 ATTAGATTTGAGTTAATAGTATGCTGTAACAGTTTATATCCAGGCC 180  
1079 ATTAGATTTGAGTTAATAGTATGCTGTAACAGTTTATATCCAGGCC 1138  
Db 181 ATGAAAAATTTAAGCTTTATAGTTTAACTTATATATTTTTCATATGTA 240  
1139 ATGAAAAATTTAAGCTTTATAGTTTAACTTATATATTTTTCATATGTA 1198  
Db 241 TTTAATCGGTATGATATTTTTCATATTTTATATATATATATATATAT 300  
1199 TTTAATCGGTATGATATTTTTCATATTTTATATATATATATATATAT 1258  
Db 301 AATTATCGGTATGATATTTTTCATATTTTATATATATATATATATAT 360  
1259 AATTATCGGTATGATATTTTTCATATTTTATATATATATATATATAT 1318

Dated

## RESULT 10

PCT-US96-12158-1

Sequence 1, Application PC/TUS9612158  
GENERAL INFORMATION:

APPLICANT: Conkling, Mark A.

APPLICANT: Mendu, Nandini

APPLICANT: Song, Wen

TITLE OF INVENTION: Root Cortex Specific Gene Promoter

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenneth D. Sibley, Bell, Seltzer, Park &amp;

ADDRESS: Gldson

STREET: Post Office Drawer 34009

CITY: Charlotte

STATE: North Carolina

COUNTRY: USA

ZIP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/12158

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Sibley, Kenneth D.

REGISTRATION NUMBER: 31,665

REFERENCE/DOCKET NUMBER: 5051-294

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-420-2200

TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2010 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US96-12158-1

Query Match

Best Local Similarity 100.0%; Score 456; DB 5; Length 2010;

Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GGAACATATTCATACATCTGCTACTGCTATATCGCTAGAACTTTGCTT 60  
959 GGAACATATTCATACATCTGCTACTGCTATATCGCTAGAACTTTGCTT 1018  
Db 61 GCTAATAAGTACTGTAATAGCTTAAATATTAATAGCATATAGATTTAGA 120  
1019 GCTAATAAGTACTGTAATAGCTTAAATATTAATAGCATATAGATTTAGA 1078  
Db 121 ATTAGATTTGAGTTAATAGTATGCTGTAACAGTTTATATCCAGGCC 180  
1079 ATTAGATTTGAGTTAATAGTATGCTGTAACAGTTTATATCCAGGCC 1138  
Db 181 ATGAAAAATTTAAGCTTTATAGTTTAACTTATATATTTTTCATATGTA 240  
1139 ATGAAAAATTTAAGCTTTATAGTTTAACTTATATATTTTTCATATGTA 1198  
Db 241 TTTAATCGGTATGATATTTTTCATATTTTATATATATATATATATAT 300  
1199 TTTAATCGGTATGATATTTTTCATATTTTATATATATATATATATAT 1318



TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSTYPIT  
 NUMBER OF INVENTION: AND USES THEREOF  
 NUMBER OF SEQUENCES: 1152  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: No. 6239264artis Corporation  
 STREET: 3054 Cornwallis Road  
 CITY: Research Triangle Park  
 STATE: No. 6239264th Carolina  
 COUNTRY: USA  
 ZIP: 27709  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/998,416  
 FILING DATE: 24-DEC-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: CH 0016/97  
 FILING DATE: 31-DEC-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meigs, J. Timothy  
 REGISTRATION NUMBER: 38,241  
 REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-541-8587  
 TELEFAX: 919-541-8689  
 INFORMATION FOR SEQ ID NO: 288:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 837 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 ORIGINAL SOURCE:  
 ORGANISM: PAG1241RP  
 US-08-998-416-288  
 Query Match 13.3% Score 60.6; DB 4; Length 837;  
 Best Local Similarity 51.1%; Pred. No. 0.00016;  
 Matches 168; Conservative 0; Mismatches 159; Indels 2; Gaps 1;

GENERAL INFORMATION:  
 APPLICANT: Blumenfeld, Marta  
 APPLICANT: Bouquellet, Lydie  
 APPLICANT: Chumakov, Ilya  
 APPLICANT: Cohen, Annick  
 TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
 TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
 FILE REFERENCE: GENSET.051CP1  
 CURRENT APPLICATION NUMBER: US/09/641,638  
 PRIOR FILING DATE: 2000-08-16  
 PRIOR APPLICATION NUMBER: US 09/502,330  
 PRIOR FILING DATE: 2000-02-11  
 PRIOR APPLICATION NUMBER: US 60/133,200  
 PRIOR FILING DATE: 1999-05-07  
 PRIOR APPLICATION NUMBER: US 09/275,267  
 PRIOR FILING DATE: 1999-03-23  
 PRIOR APPLICATION NUMBER: US 60/119,917  
 PRIOR FILING DATE: 1999-02-12  
 NUMBER OF SEQ ID NOS: 1304  
 SOFTWARE: Patent.pm  
 SEQ ID NO 651  
 LENGTH: 20674  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 1123..3123  
 OTHER INFORMATION: 5' regulatory region  
 NAME/KEY: exon  
 LOCATION: 3124..3297  
 OTHER INFORMATION: exon 1  
 NAME/KEY: exon  
 LOCATION: 3871..4072  
 OTHER INFORMATION: exon 2  
 NAME/KEY: exon  
 LOCATION: 5552..5633  
 OTHER INFORMATION: exon 3  
 NAME/KEY: exon  
 LOCATION: 5758..5880  
 OTHER INFORMATION: exon 4  
 NAME/KEY: exon  
 LOCATION: 5996..6099  
 OTHER INFORMATION: exon 5  
 NAME/KEY: exon  
 LOCATION: 6349..6509  
 OTHER INFORMATION: exon 6  
 NAME/KEY: exon  
 LOCATION: 7379..7522  
 OTHER INFORMATION: exon 7  
 NAME/KEY: exon  
 LOCATION: 8645..8854  
 OTHER INFORMATION: exon 8  
 NAME/KEY: exon  
 LOCATION: 12254..12340  
 OTHER INFORMATION: exon 9  
 NAME/KEY: exon  
 LOCATION: 12854..13023  
 OTHER INFORMATION: exon 10  
 NAME/KEY: exon  
 LOCATION: 13308..13429  
 OTHER INFORMATION: exon 11  
 NAME/KEY: exon  
 LOCATION: 16567..16667  
 OTHER INFORMATION: exon 12  
 NAME/KEY: exon  
 LOCATION: 16775..16945  
 OTHER INFORMATION: exon 13  
 NAME/KEY: exon  
 LOCATION: 17063..17554  
 OTHER INFORMATION: exon 14  
 NAME/KEY: misc\_feature  
 LOCATION: 17555..20674  
 OTHER INFORMATION: 3' regulatory region

```

1 OTHER INFORMATION: 10-347-165 : polymorphic base C or T
2 NAME/KEY: allele
3 LOCATION: 6467
4 OTHER INFORMATION: 10-347-203 : polymorphic base A or G
5 NAME/KEY: allele
6 LOCATION: 6484
7 OTHER INFORMATION: 10-347-220 : polymorphic base A or G
8 NAME/KEY: allele
9 LOCATION: 6534
10 OTHER INFORMATION: 10-347-271 : polymorphic base A or T
11 NAME/KEY: allele
12 LOCATION: 6611
13 OTHER INFORMATION: 10-347-348 : polymorphic base A or G
14 NAME/KEY: allele
15 LOCATION: 7668
16 OTHER INFORMATION: 10-348-391 : polymorphic base A or G
17 NAME/KEY: allele
18 LOCATION: 8608
19 OTHER INFORMATION: 10-349-47 : polymorphic base C or T
20 NAME/KEY: allele
21 LOCATION: 8658
22 OTHER INFORMATION: 10-349-97 : polymorphic base A or G
23 NAME/KEY: allele
24 LOCATION: 8703
25 OTHER INFORMATION: 10-349-142 : polymorphic base G or C
26 NAME/KEY: allele
27 LOCATION: 8777
28 OTHER INFORMATION: 10-349-216 : deletion of CTG
29 NAME/KEY: allele
30 LOCATION: 8785
31 OTHER INFORMATION: 10-349-224 : polymorphic base G or T
32 NAME/KEY: allele
33 LOCATION: 8926
34 OTHER INFORMATION: 10-349-368 : polymorphic base C or T
35 NAME/KEY: allele
36 LOCATION: 12171
37 OTHER INFORMATION: 10-350-72 : polymorphic base C or T
38 NAME/KEY: allele
39 LOCATION: 12429
40 OTHER INFORMATION: 10-350-332 : polymorphic base C or T
41 NAME/KEY: allele
42 LOCATION: 13341
43 OTHER INFORMATION: 10-507-170 : polymorphic base A or G
44 NAME/KEY: allele
45 LOCATION: 13482
46 OTHER INFORMATION: 10-507-321 : polymorphic base A or C
47 NAME/KEY: allele
48 LOCATION: 13524
49 OTHER INFORMATION: 10-507-353 : polymorphic base C or T
50 NAME/KEY: allele
51 LOCATION: 13535
52

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QY	51	TTTGGCTGGCTAAATAACATCTGGAATGACCTAGTTAAATTAATTAATGCAATAA	110
Db	11064	TTTTTTTAATAGCTAAGAAATAATTTTAATTTTAAATTTTAATAATTTTAATTAATA	11123
QY	111	GATTTAGCATATGATTTTGAAGTTAATCTATAGACTGTAAACAGTTTTATAAT	170
Db	11124	TTAAATTAATAATTTTAATTTAATATATTAATTAATTTTAATTTTAATAATAATTA	11183
QY	171	TCCAAGGCCCATGAAAAATTTAATGCTTTATTAGTTTAACTACTAATATAATTTTC	230
Db	11184	AATTTAATAATTAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAACATTTAAATTTT	11243
QY	231	AATATGTAATAATTTAATGCGTATAGTGCATATTTTTCATATTTATTTATAAATAA	290
Db	11244	AATTTTATATTAATTAATTAATTTAATTAATTAATTAATTAATTAATTAATTAATTA	11303

OY 291 ACTTACCTTATATGCGTACGTATAGATTATATATAAAATCTACGGTCTTCAGAA 350  
DB 11304 ATTACTTAAATTTAAATTAATTAATTAATTAATTAATTTTAAATTTTAAATA 11363  
OY 351 GAACCTTA 359  
DB 11364 TTAATTTTA 11372

## RESULT 15

US-08-998-416-1137

Sequence 1137 Application US/08998416

Patent No. 6239264

GENERAL INFORMATION:

APPLICANT: Philippesen, Peter

APPLICANT: Pohlmann, Rainer

APPLICANT: Steiner, Sabine

APPLICANT: Mohr, Christine

APPLICANT: Wendland, Jurgen

APPLICANT: Knechtle, Philipp

APPLICANT: Redischung, Corline

TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPII

NUMBER OF SEQUENCES: 1152

CORRESPONDENCE ADDRESS:

ADDRESS: No. 6239264artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: No. 6239264th Carolina

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/998,416

FILING DATE: 24-DEC-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CH 0016/97

FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Melgs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976

TELEPHONE: 919-541-8587

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 1137:

SEQUENCE CHARACTERISTICS:

LENGTH: 636 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: PAC1692RP

US-08-998-416-1137

Query Match 12.28; Score 55.6; DB 4; Length 636;

Best Local Similarity 52.18; Pred. No. 0.0016;

Matches 148; Conservative 0; Mismatches 134; Indels 2; Gaps 1;

OY 124 AGTATTTGAGTTTAAATTAATTAATG--ACTGTACAGTTTAAATTCAGGCCA 181  
DB 354 TAAAGATTAAATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 413  
OY 182 TGAATAATTTAAATCTTTAGTTTAAACTTCTATTAATTTTCAATGTAAT 241  
DB 414 TAAATATTATGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 473  
OY 242 TTAATCGTATAGTTGATATTTTTCATTTATTTTAAATAA 285  
DB 474 TTAATCTTAATTTCTTATTAATTAATTTTATTAATTAATTA 517

Search completed: June 9, 2003, 08:04:35  
Job time : 46 secs

OY 4 AACATATCAATGATGTTGCTACATATATCGCTAGAAATCTTGCGCTTGTCT 63  
DB 234 AAATTAATTTAAATTAATTAATTAATTAATTTTCTTAATTAATTAATTA 293  
OY 64 AATAAGATCTGAAATAGCTTAAATATAAATAGCATATAGATTTGGAATT 123  
DB 294 TTAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 353



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 07:10:45 ; Search time 125 Seconds  
(Without alignments)  
5105.512 Million cell updates/sec

Title: US-09-941-042C-1

Perfect score: 456  
Sequence: 1 ggaacatactacatacatt.....ggttaaaagcgttacagag 456

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_NA:\*  
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11: /cgn2\_6/ptodata/1/pubpna/US10\_NEM\_PUB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEM\_PUB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	58.2	12.8	858	9	US-10-198-846-7035
2	57	12.5	53332	9	US-10-224-562-3
3	57	12.5	53332	10	US-09-801-861-3
4	54.4	11.9	6327	9	US-10-239-676-151
5	53.6	11.8	14078	7	US-08-781-986A-191
6	53.6	11.7	513509	9	US-09-754-853A-4
7	53.4	11.7	272	10	US-09-969-373-607
8	53.4	11.7	272	10	US-09-969-373-608
9	53	11.6	6030	9	US-10-239-676-164
10	53	11.6	15732	9	US-10-239-676-164
11	52.8	11.6	11047	9	US-10-239-676-187
12	52.6	11.5	3991	9	US-10-074-045-60
13	52.4	11.5	4985	9	US-10-094-240-10
14	52.2	11.4	3991	9	US-10-074-045-60
15	52	11.4	376	10	US-09-960-352-5087
16	51.6	11.3	64081	10	US-09-790-988-1
17	51.4	11.3	7380	9	US-10-239-676-66
18	51.4	11.3	17421	9	US-10-239-676-54
19	51.2	11.2	2000	9	US-09-938-842A-3652

20	50.6	11.1	9515	9	US-10-239-676-159	Sequence 159, App
21	50.4	11.1	640681	10	US-09-790-988-1	Sequence 1, Appl
22	50.2	11.0	7823	9	US-10-239-676-197	Sequence 197, Appl
23	50	11.0	419	10	US-09-960-352-11234	Sequence 11234, A
24	50	11.0	5689	9	US-10-239-676-90	Sequence 90, Appl
25	49.6	10.9	414	10	US-09-960-352-6528	Sequence 6528, App
26	49.6	10.9	437	10	US-09-969-373-937	Sequence 937, Appl
27	49.6	10.9	335913	9	US-09-754-853A-2	Sequence 2, Appl
28	49.6	10.9	335913	9	US-09-754-853A-3	Sequence 3, Appl
29	49.4	10.8	424	9	US-10-198-846-2929	Sequence 2929, App
30	49.4	10.8	11036	9	US-10-239-676-118	Sequence 118, App
31	49.4	10.8	15732	9	US-10-239-676-95	Sequence 95, Appl
32	49.4	10.8	15732	9	US-10-239-676-96	Sequence 96, Appl
33	49	10.7	960	9	US-10-198-846-5381	Sequence 6381, App
34	49	10.7	4187	9	US-10-072-349-252	Sequence 252, App
35	49	10.7	4187	10	US-09-764-855-252	Sequence 252, App
36	48.8	10.7	5979	9	US-10-239-676-18	Sequence 18, Appl
37	48.8	10.7	6306	9	US-10-239-676-223	Sequence 223, App
38	48.8	10.7	7038	9	US-10-239-676-204	Sequence 204, Appl
39	48.8	10.7	7038	9	US-10-060-036-256	Sequence 256, App
40	48.6	10.7	714	9	US-10-239-676-67	Sequence 67, Appl
41	48.6	10.7	7089	9	US-10-239-676-71	Sequence 71, Appl
42	48.6	10.7	8842	9	US-10-239-676-36	Sequence 36, Appl
43	48.6	10.7	12405	9	US-10-239-676-36	Sequence 3976, App
44	48.4	10.6	12003	10	US-09-764-877-3976	Sequence 3976, App
45	48.4	10.6	30350	9	US-10-118-328-3	Sequence 3, Appl

#### ALIGNMENTS

RESULT 1  
US-10-198-846-7035/C  
Sequence 7035, Application US/10198846  
Publication No. US200309974A1  
GENERAL INFORMATION:  
APPLICANT: Lillie, James  
APPLICANT: Xu, Yongyao  
APPLICANT: Wang, Youzhen  
TITLE OF INVENTION: STEINMANN, Kathleen  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
FILE REFERENCE: MRI-049  
CURRENT APPLICATION NUMBER: US/10/198,846  
CURRENT FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/306,220  
PRIOR FILING DATE: 2001-07-18  
NUMBER OF SEQ ID NOS: 14084  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7035  
LENGTH: 858  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 137, 182, 183, 184, 185, 186, 187, 188, 209, 211, 212, 217  
LOCATION: 219, 224, 225, 236, 237, 238, 240, 241, 242, 248, 250, 252  
LOCATION: 253, 259, 276, 279, 281, 298, 298, 304, 306, 318, 319  
LOCATION: 320, 321, 327, 338, 349, 350, 352, 355, 363, 378, 379  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 380, 386, 389, 392, 398, 399, 400, 408, 410, 414, 434, 441  
LOCATION: 443, 446, 451, 455, 466, 488, 490, 497, 498, 499, 501, 503  
LOCATION: 506, 509, 513, 517, 526, 527, 528, 529, 536, 550, 557, 562  
LOCATION: 564, 565, 573, 576, 588, 599, 604, 607, 616, 617, 619  
OTHER INFORMATION: n = A,T,C or G  
FEATURE:  
NAME/KEY: misc-feature  
LOCATION: 627, 628, 643, 649, 661, 666, 672, 680, 689, 706, 719  
LOCATION: 722, 735, 739, 750, 763, 765, 769, 771, 772, 774, 784, 787  
LOCATION: 790, 791, 792, 795, 798, 805, 814, 816, 819, 820, 822, 830



OY 242 TTAATCGTATAGTGCATATTTTCAATTTATATAA 285  
| | | | | | | | | | | | | | | | | | | |  
Db 136241 ATTGCATTTTATGCTATTAATGACATTTGTTATCATATATA 136198

## RESULT 7

US-09-969-373-607/c  
Sequence 607, Application US/09969373  
Patent No. US2002013852A1  
GENERAL INFORMATION:  
APPLICANT: Effertz, Roger J.  
APPLICANT: Haugue, Brian M.  
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
FILE REFERENCE: 38-10(52679)A  
CURRENT APPLICATION NUMBER: US/09/969,373  
CURRENT FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: US 09/754,853  
PRIOR FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: US 09/760,427  
PRIOR FILING DATE: 2001-01-13  
PRIOR APPLICATION NUMBER: US 09/855,768  
PRIOR FILING DATE: 2001-05-15  
NUMBER OF SEQ ID NOS: 4593  
SEQ ID NO 607  
LENGTH: 272  
TYPE: DNA  
ORGANISM: Glycine max  
US-09-969-373-607

Query Match 11.7%; Score 53.4; DB 10; Length 272;  
Best Local Similarity 50.6%; Pred. No. 1.1;

Matches 129; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

OY 90 TTAATATTAATACATATATATTTAGATTTGATTTGATTTAATTTATG 149  
| | | | | | | | | | | | | | | | | | | |  
Db 255 TTAATATTAATATTTATTTATTTATTTATTTATTTATTTATTTATTTA 196  
| | | | | | | | | | | | | | | | | | | |  
OY 150 ACTGTACAGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 209  
| | | | | | | | | | | | | | | | | | | |  
Db 195 AATTAATATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 136  
| | | | | | | | | | | | | | | | | | | |  
OY 210 AACTTACTATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTA 269  
| | | | | | | | | | | | | | | | | | | |  
Db 135 TTAATTTTAAATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTA 76  
| | | | | | | | | | | | | | | | | | | |  
OY 270 ATTATTTTAAATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTA 329  
| | | | | | | | | | | | | | | | | | | |  
Db 75 AACATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 16  
| | | | | | | | | | | | | | | | | | | |  
OY 330 AAAATCTACGTTCT 344  
| | | | | | | | | | | | | | | | | | | |  
Db 15 ACATTGAAGTTTCT 1

## RESULT 8

US-09-969-373-608/c  
Sequence 608, Application US/09969373  
Patent No. US2002013852A1  
GENERAL INFORMATION:  
APPLICANT: Effertz, Roger J.  
APPLICANT: Haugue, Brian M.  
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
FILE REFERENCE: 38-10(52679)A  
CURRENT APPLICATION NUMBER: US/09/969,373  
CURRENT FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: US 09/754,853  
PRIOR FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: US 09/760,427  
PRIOR FILING DATE: 2001-01-13  
PRIOR APPLICATION NUMBER: US 09/855,768  
PRIOR FILING DATE: 2001-05-15  
NUMBER OF SEQ ID NOS: 4593

; SEQ ID NO 608  
; LENGTH: 272  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-969-373-608

Query Match 11.7%; Score 53.4; DB 10; Length 272;  
Best Local Similarity 50.6%; Pred. No. 1.1;

Matches 129; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

OY 90 TTAATATTAATACATATATTTAGATTTGATTTGATTTAATTTATG 149  
| | | | | | | | | | | | | | | | | | | |  
Db 255 TTAATATTAATATTTATTTATTTATTTATTTATTTATTTATTTATTTA 196  
| | | | | | | | | | | | | | | | | | | |  
OY 150 ACTGTACAGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 209  
| | | | | | | | | | | | | | | | | | | |  
Db 195 AATTAATATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 136  
| | | | | | | | | | | | | | | | | | | |  
OY 210 AACTTACTATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTA 269  
| | | | | | | | | | | | | | | | | | | |  
Db 135 TTAATTTTAAATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTA 76  
| | | | | | | | | | | | | | | | | | | |  
OY 270 ATTATTTTAAATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTA 329  
| | | | | | | | | | | | | | | | | | | |  
Db 75 AACATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 16  
| | | | | | | | | | | | | | | | | | | |  
OY 330 AAAATCTACGTTCT 344  
| | | | | | | | | | | | | | | | | | | |  
Db 15 ACATTGAAGTTTCT 1

## RESULT 9

US-10-239-676-164  
Sequence 164, Application US/10239676  
Publication No. US20030082609A1  
GENERAL INFORMATION:  
APPLICANT: OLER, Alexander  
APPLICANT: PIEPENBROCK, Christian  
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation  
FILE REFERENCE: 5013.1003  
CURRENT APPLICATION NUMBER: US/10/239,676  
CURRENT FILING DATE: 2002-09-24  
PRIOR APPLICATION NUMBER: PCT/EP01/03968  
DE 10019058.8  
DE 10019173.8  
DE 10032528.7  
DE 10043826.1  
PRIOR FILING DATE: 2001-04-06  
2000-04-06  
2000-04-07  
2000-06-30  
2000-09-01  
NUMBER OF SEQ ID NOS: 228  
SEQ ID NO 164  
LENGTH: 6030  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
NAME/KEY: unsure  
LOCATION: (5455)  
US-10-239-676-164

Query Match 11.6%; Score 53; DB 9; Length 6030;  
Best Local Similarity 48.0%; Pred. No. 3.2;

Matches 181; Conservative 0; Mismatches 195; Indels 1; Gaps 1;

OY 80 ATAGCTAGTTTAATTAATTAATGCAATTAATGATTTTGAATTTAGATTTTGA 139  
| | | | | | | | | | | | | | | | | | | |  
Db 704 ATGATTTTATTAATGTTGTTTATTTTATTTTGAATTAAGAAATTTGATTTTGA 763



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; LENGTH: 376
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 22-LIB3058-032-Q1-K1-F9
US-09-960-352-5087

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Query Match      11.48; Score 52; DB 10; Length 376;
Best Local Similarity 52.38; Pred. No. 2.1;
Matches 115; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

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QY 68 AAGTACTGTGAATAGCTAGTTAAATATAATAGCATATAGATTTTAGAATTAGTA 127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 100 AATATTAATTTTATTTATTTACATTTGATTTTAAATTTTAAATTTTGATTTATAA 159
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 128 TTTGAGCTTAACTTAACTGATGCTGTAACAGTTTAAATTTCAAGCCCATGAAAA 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 160 TTTTATTTTATTTATTTATTTTGTATTTATTTTATTTTATTTATTTATTTAT 219
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 188 ATTTAATGCTTTATTTAGTTTAACTTAACTTAAATTTTCAATGTAATAATTTAATC 247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 220 TTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 279
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 248 GGTATAGTTCATATTTTTCATTTTCAATTTTATTTATAAATA 287
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 280 ATTTATATTTATTTTATTTTATTTTATTTTATTTTATTTATTA 319
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Job time : 127 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 07:10:15 ; Search time 1128 Seconds  
(Without alignments)  
6547.112 Million cell updates/sec

Title: US-09-941-042C-1  
Perfect score: 456  
Sequence: 1 ggaacataatcatacatc.....gtaaaagcagttacagag 456

Scoring table: IDENTITY\_MNC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: \*  
1: em\_estba: \*  
2: em\_esthu: \*  
3: em\_estin: \*  
4: em\_estnu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_htc: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_htc: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: gb\_gss: \*  
18: em\_gss\_hum: \*  
19: em\_gss\_inv: \*  
20: em\_gss\_pln: \*  
21: em\_gss\_vtc: \*  
22: em\_gss\_fun: \*  
23: em\_gss\_mam: \*  
24: em\_gss\_mus: \*  
25: em\_gss\_other: \*  
26: em\_gss\_pro: \*  
27: em\_gss\_rtd: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	75.2	16.5	1101 17	CNS00FYG AL071206 Drosophila
2	74.8	16.4	905 17	CNS00KHX AL077798 Drosophila
3	73.2	16.1	928 17	CNS00DKY AL071865 Drosophila
4	72.6	15.9	976 17	CNS04ESM AL286627 Tetradon
5	72.6	15.9	1101 17	CNS00EVL AL069706 Drosophila
6	72.6	15.9	1225 17	CNS0161D AL106171 Drosophila

Result No.	Score	Query Length	DB ID	Description
7	72	15.8	928 17	CNS00DKY AL071865 Drosophila
8	71.2	15.6	1101 17	CNS0014P AL104456 Drosophila
9	70.2	15.4	1101 17	CNS0016L AL078714 Drosophila
10	69.2	15.2	1043 17	CNS0145P AL106896 Drosophila
11	68.4	15.0	987 17	CNS0145P AL103735 Drosophila
12	68.4	15.0	987 17	CNS0145P AL104456 Drosophila
13	68.4	15.0	1203 17	CNS015W Drosophila
14	68.2	15.0	1101 17	CNS001E Drosophila
15	68	14.9	1101 17	CNS001E Drosophila
16	67.6	14.8	524 17	CNS010Y Drosophila
17	67	14.7	662 12	BG592447 EST612295
18	67	14.7	740 17	BQ504880 EST612295
19	66.4	14.6	1101 17	CNS00D7 Drosophila
20	66.2	14.5	795 17	BH460882 BGF84TF
21	66.2	14.5	814 17	BH695520 BOMN06TR
22	66.2	14.5	1001 17	CNS0155H AL105023 Drosophila
23	66	14.5	945 17	CNS04DOK AL285149 Tetradon
24	66	14.5	1101 17	CNS002ZU AL097152 Drosophila
25	65.8	14.4	843 17	CNS00CS1 AL059666 Drosophila
26	65.4	14.3	769 17	CNS005XX AL062647 Drosophila
27	65.2	14.3	660 17	BH183498 023_L_07-AL620449 T3 end of
28	65.2	14.3	660 17	CNS070N Drosophila
29	65	14.3	876 17	CNS0096L AL053529 Drosophila
30	65	14.3	1101 17	CNS00EVL AL068706 Drosophila
31	64.6	14.2	1101 17	CNS016L AL108896 Drosophila
32	64.2	14.1	1092 17	CNS020K7 AL175696 Tetradon
33	64.2	14.1	1101 17	CNS004EW AL055440 Drosophila
34	64.2	14.1	1101 17	CNS003BD AL064091 Drosophila
35	63.8	14.0	752 17	BH693739 BOMG68TF
36	63.8	14.0	843 17	CNS00CS1 AL059666 Drosophila
37	63.8	14.0	883 17	A2550845 ENTF51TF
38	63.8	14.0	1184 17	AL300845 Tetradon
39	63.6	13.9	1027 17	CNS04P4P AL212733 Tetradon
40	63.6	13.9	1101 17	CNS001E AL060732 Drosophila
41	63.6	13.9	1101 17	CNS00YWL AL098927 Drosophila
42	63.6	13.9	1200 17	CNS016C0 AL106578 Drosophila
43	63.4	13.9	975 17	BH179465 014_P_10-AL069440 Drosophila
44	63.4	13.9	1101 17	CNS00E07 AL106121 Drosophila
45	63.4	13.9	1201 17	CNS0152Z

## ALIGNMENTS

RESULT 1  
CNS00FYG  
LOCUS  
DEFINITION  
Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR32N04 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
ACCESSION  
AL071206  
AL071206.1 GI:4951245  
VERSION  
GSS.  
KEYWORDS  
Drosophila melanogaster.  
SOURCE  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
ORGANISM  
1 (bases 1 to 1101)  
REFERENCE  
Genoscope.  
AUTHORS  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
TITLE  
JOURNAL  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuhiro Oseogawa and Aaron Mammose in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial









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: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PT221C1
: CURRENT APPLICATION NUMBER: US/10/074,045
: CURRENT FILING DATE: 2002-02-14
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 74
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 60
: LENGTH: 3391
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-074-045-60

```

	Query Match Best Local Similarity	11.5%, 52.0%,	Score 52.6; Pred. No. 3.3	DB 9;	Length 3991;
	Matches 143;	Conservative 0;	Mismatches 129;	Indels 3;	Gaps 1
QY	78	AAATAGCTTACTTTAAATATTAATAGCATTAATAGATTTTTCAGAAATTTAGATTTTGAGTTT	137		
DB	3106	AAATATATTAAGCCATATATTTAAATTAATATATTTATTTATTTATTTATTTAAATAAATATA	3165		
QY	138	AATTACTTAATGACGTCTTAACAGTTTATATATTCAGGCCATGAAATAATTAATGCT	197		
DB	3166	TATTTATTTTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	3222		
QY	198	TTATTAAGTTTAAACTTACTATTAATATTTTCATATGCTAAATTTAAATTCGATATAGTTC	257		
DB	3226	TTTATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT	3285		
QY	258	GATTTTTTTTCAATTTATTT--TTTAAATTAATAAAAAACTCAACCTAATTTATTCGGTACAG	314		
DB	3286	ATAAATTAATTAATTTATTAATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	3345		
QY	315	TTATAGTTTATATATAAAATCTACGGTCTTCACA	349		
DB	3346	AAATATATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	3380		

```

RESULT 13
US-10-094-240-10
: Sequence 10. Application US/10094240
: Publication NO. US20030082637A1
: GENERAL INFORMATION:
: APPLICANT: ZWIEBEL, LAURENCE J.
: TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
: FILE REFERENCE: N8289
: CURRENT APPLICATION NUMBER: US/10/094,240
: CURRENT FILING DATE: 2001-03-08
: PRIOR APPLICATION NUMBER: 10/056,405
: PRIOR FILING DATE: 2002-01-24
: PRIOR APPLICATION NUMBER: 60/264,649
: PRIOR FILING DATE: 2001-01-26
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 10
: LENGTH: 4985
: TYPE: DNA
: ORGANISM: Anopheles gambiae
: US-10-094-240-10

```

	Query Match	11.5%	Score 52.4	DB 9	Length 4985	
	Best Local Similarity	49.0%	Pred. No. 3.8			
	Matches 140; Conservative	0;	Mismatches 146;	Indels	0;	Gaps 0;
OY	33 TCATAAACCGTAGATACTTTGTGCGCTTGCCTAATAAAGACTCTGAATAGCCTTAGTTTA	92				
Dd	2726 TATTATACCAATATATATATTTATATANGATTATTTATTTATTTATATATATATATAT	2785				
OY	93 AATATAATAGCATATATAGATTTTGGAAATAGATTGTCATTAATCTATAGACT	152				
Dd	2786 TATTATATATATATATCTTATTTATATATATATATATATATATTTAATAATATATTTTAA	2845				

[illegible]

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RESULT 14
US-10-074-045-60/c
: Sequence 60, Application US/10074045
: Publication No. US20030092102A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PIZ21C1
: CURRENT APPLICATION NUMBER: US/10/074,045
: PRIOR FILING DATE: 2002-02-14
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 74
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 60
: LENGTH: 3991
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-074-045-60

```

	Query Match	11.4%	Score 52.2	DB 9	Length 3991
	Best Local Similarity	52.5%	Pred. No. 3.9		
	Matches 137	Conservative 0	Mismatches 123	Indels 1	Gaps 1
QY	78	AAATAGCTTGAGTTAAATATATAATAGCATATAGATTTTGAAGATTGATTTTGAGCTT	137		
Db	3355	AAATATATTTATATATATAATTAATAATATATAATATTTTAAATATATTAAATAT	3296		
QY	138	AATTACTATTGACCTGTACAGCTTTTATATATCCAGGCCATGAAAAATTTAAATGCT	197		
Db	3295	ATTATATTTAAATATATAATATATATTTTATTAATATATAATATATATATATTTAT	3236		
QY	198	TTTATAGCTTTA-ACTTACTATATATAATTTTCATATGTAATAATTAAACGGTATGCT	256		
Db	3235	AAATTAATAAATATATATTTTATTAATAATATAATATATATTTATTTATTTAAATTA	3176		
QY	257	CGATATTTTTCATATATATTTTATAAATAAATAAAGCTACCCATATATCGGACAGT	316		
Db	3175	TAAATAAATATATATTTATTTAATAAATATAAATAAATATATATTTTATATATATGCG	3116		
QY	317	ATAGATTATATAAATACTA	337		
Db	3115	TTATATATTTATTTATATATA	3095		

RESULT 15  
 US-09-960-352-5087  
 ; Sequence 5087, Application US/09960352  
 ; Patent No. US20020137139A1  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Warren, Wesley C.  
 ;  
 ; APPLICANT: Tao, Mengling  
 ;  
 ; APPLICANT: Byatt, John C.  
 ;  
 ; APPLICANT: Mathialagan, Nagappan  
 ;  
 ; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
 ;  
 ; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION  
 ;  
 ; FILE REFERENCE: 16511.006/37-21(10298)C  
 ;  
 ; CURRENT APPLICATION NUMBER: US/09/960,352  
 ;  
 ; CURRENT FILING DATE: 2001-09-24  
 ;  
 ; NUMBER OF SEQ ID NOS: 15112  
 ;  
 ; SEQ ID NO 5087

BASE COUNT	277	a	96	c	121	g	362	t	167	others
ORIGIN										

[illegible]

	RESULT 12
CNS014PQ/c	
LOCUS	987 bp DNA linear GSS 26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence sp6 end of BAC BACN1P22 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL104456
VERSION	ALI04456.1 GI:5616067
KEYWORDS	GSS.
SOURCE	Drosophila melanogaster.
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Epiphytoidae; Drosophilidae; Drosophila. 1 (bases 1 to 987) Genoscope.
REFERENCE	Direct Submission
AUTHORS	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segrete@genoscope.cns.fr
JOURNAL	- Web : www.genoscope.cns.fr)
TITLE	determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <a href="http://www.edgp.ebi.ac.uk/">http://www.edgp.ebi.ac.uk/</a> . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CDPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pbeloBAC11.
COMMENT	

```

FEATURES
  source
    location/Qualifiers
      1. 987
        /organism="Drosophila melanogaster"
        /db_xref="taxon:7227"
        /clone="BACN12P22"
        /clone_1fb="DrosBAC"
        /plasmid="pbeloBac11"
        /note="end : Sp6"

```

BASE COUNT	257 a	122 c	122 g	241 t	245 others
ORIGIN					

Query Match	15.0%	Score 68.4	DB 17	length 987
Best Local Similarity	30.3%	Pred. No. 0.014		
Matches 117, Conservative	104	Mismatches	161	Indels 4, Gaps 1

OY	63	TAATAAAGACTGCGAATPAGCTGTGGTTAAATAGCATATAGATTGTAAGCAT	122
		.....:     :         :     :     :     :     :     :     :     :	
Db	951	WMMWMMWMTTTTTTTTWTTTTTTTTTTTTAAATTAATWMMWMMHHHTTTHMMWMTWT	892
OY	123	TAGATATTGTAGTTTAATTACTATTGACTGTACAAGTTTTTATTAATTCAGGCCCAT	182
		:     :       :     :     :     :     :     :     :     :	
Db	891	WMAATWTTTMAATTWMMWMCWATTTWTWMMWMAATTTATWMAAAAAAAMWMAW	832
OY	183	GAAAAATTAATGCTTTATTAGTTTAAACCTACATATAATTTTTCATATAGTAA----	238
		:   :     :     :     :     :     :     :     :     :     :	
Db	831	MTNTAWMAMWTATTAATTWMMATWMAATWMAATWMAATTAATTAATWMAAAAAATTTW	772
OY	239	AATTAATCGGATATGTCGATATTTTTCAATTTATTTTAAAAATTAANAACCTACC	298
		:       :     :     :     :     :     :     :	
Db	771	AATTAATAAAMTTTCTTTTAAAMWATWMAWMAWTTTWTWTWTBTTTAAAAA	712
OY	299	CTAATTAATCGGACAGTTATAGATTATATAAATACTACGGTCTTCAGAGAAACCTA	358
		.....:     :       :     :     :     :     :     :     :	
Db	711	WAMWMMWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAW	652
OY	359	AAATCGGTCGGTCGGACGCTGCATCGGTTAGTCGATTTTCAAAATATTCATGACA	418
		:   :   :   :   :     :     :     :     :     :     :     :	
Db	651	WTKMTTKTKTKTKTKKGGGGGGGGGVAWVKRMAAAAAAAAAAAMMMMMMMMMV	592
OY	419	CTCCGATGTGTATAGTAAAAA	444
		.....:     :           :     :     :     :     :	
Db	591	YYYYYHHTTWTWTCTTAAAMH	566

RESULT 13  
CNS015MW  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CNS015MW 1203 bp DNA linear GSS 26-JUL-1999  
Drosophila melanogaster genome survey sequence Sp6 end of BAC  
BA0N1510 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
AL106008  
AL106008.1 GI:5619558  
GSS.  
Drosophila melanogaster.  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1203)  
Genoscope.  
Direct Submission  
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage ; :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr)  
- Web : www.genoscope.cns.fr)  
determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC  
library (Dros BAC) was made by Alain Billaud at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
pBelobAC11.

FEATURES	Location/Qualifiers
source	1..1203
	/organism="Drosophila melanogaster"
	/db_xref="taxon:7227"
	/clone="BACN15E10"
	/clone_1lb="DrosBAC"
	/plasmid="pbelBAC11"
	/note="end : Sp6"
BASE COUNT	288 a 103 c 235 g 253 t 324 others







PL and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

1. 1101  
Location/Qualifiers  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone="BACR29B23"  
/clone\_11b="RPCI-98"  
/note="end : 77"

BASE COUNT 419 a 91 c 60 g 299 t 232 others  
ORIGIN

Query Match 15.9%; Score 72.6; DB 17; Length 1101;  
Best Local Similarity 35.1%; Pred. No. 0.0027;  
Matches 150; Conservative 74; Mismatches 203; Indels 0; Gaps 0;

OY 4 AACATATTCATACCTGTTAGTTCGTCATTAATCGCTAGAAATACCTGCTGCT 63  
DB 1082 WMTATWTTAAAT 1023  
OY 64 AATAAGATCTGAAATAGCTAGTTAAATATATATATATATATATATATATAT 123  
DB 1022 AT 963  
OY 124 AGTATTTGAGTTATATATATATATATATATATATATATATATATATATAT 183  
DB 962 WMTATWTTAAAT 903  
OY 184 AAAAAATTAATGCTTTATAGTTTAACTATATATATATATATATATATATAT 243  
DB 902 TATWTTWAAAAAAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAM 843  
OY 244 AATCGGTAGTGCATATATATATATATATATATATATATATATATATATAT 303  
DB 842 WMTAT 783  
OY 304 TATCGGTAGTGCATATATATATATATATATATATATATATATATATATAT 363  
DB 782 WMTWTTWAAAAAAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAM 723  
OY 364 CGGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 423  
DB 722 ATWTTATWTTTATWTTTATWTTTATWTTTATWTTTATWTTTATWTTTAT 663  
OY 424 AGTGTG 430  
DB 662 AATTATT 656

RESULT 6  
CNS0161D 1225 bp DNA linear GSS 26-JUL-1999  
LOCUS  
DEFINITION Drosophila melanogaster genome survey sequence Sp6 end of BAC  
BACN15C18 of Drosophila library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION  
VERSION AL106171.1 GI:5620504  
KEYWORDS  
SOURCE GSS  
ORGANISM Drosophila melanogaster.  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  
1 (bases 1 to 1225)

AUTHORS  
TITLE Direct Submission  
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequefgenoscope.cns.fr  
- web : www.genoscope.cns.fr)

COMMENT Determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -

<http://www.edgp.ebi.ac.uk> - . This Drosophila melanogaster BAC  
library (Dros BAC) was made by Alain Billard at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
pBelobAC11.

## FEATURES

source

1. 1225  
Location/Qualifiers  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone="BACN15C18"  
/clone\_11b="DrosBAC"  
/plasmid="pBelobAC11"  
/note="end : 56"

BASE COUNT 266 a 128 c 38 g 368 t 425 others  
ORIGIN

Query Match 15.9%; Score 72.6; DB 17; Length 1225;  
Best Local Similarity 37.4%; Pred. No. 0.0026;  
Matches 114; Conservative 61; Mismatches 130; Indels 0; Gaps 0;

OY 60 TGCTAATAAGTACTGAAATAGCTTAAATATATATATATATATATATATATAT 119  
DB 902 TTTTAT 961  
OY 120 AATAGTATTTGAGTTATATATATATATATATATATATATATATATATATAT 179  
DB 962 WMTAAAT 1021  
OY 180 CATGAAAAATTAATGCTTTATAGTTTAACTATATATATATATATATATATAT 239  
DB 1022 WAAAAAATAAT 1081  
OY 240 AATTATCGTATAGTGCATATATATATATATATATATATATATATATATATAT 299  
DB 1082 WMTATWTTTATWTTTATWTTTATWTTTATWTTTATWTTTATWTTTATWTT 1141  
OY 300 TAATTATCGTACCTATATATATATATATATATATATATATATATATATATAT 359  
DB 1142 TWTWTTWAAAAAAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAM 1201  
OY 360 AATC 364  
DB 1202 AATAT 1206

RESULT 7  
CNS00DKY 928 bp DNA linear GSS 04-JUN-1999  
LOCUS  
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC  
BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION  
VERSION AL071865.1 GI:4948170  
KEYWORDS  
SOURCE GSS  
ORGANISM Drosophila melanogaster.  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  
1 (bases 1 to 928)

AUTHORS  
TITLE Direct Submission  
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequefgenoscope.cns.fr  
- web : www.genoscope.cns.fr)

COMMENT Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> The BDGP Drosophila  
melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
Aron Mammoser in Pieter de Jong's laboratory in the Department of



NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y<sup>+</sup>; cn bw sp, the same strain used for the BDGP, P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACRAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES	Location/Qualifiers
source	1. .1101

BASE COUNT	469 a	6 c	69 g	151 t	406 others
ORIGIN					

Query Match	15.68;	Score 71.2;	DB 17;	Length 1101;
Best Local Similarity	32.48;	Pred. No. 0.0046;		
Matches 127;	Conservative 101;	Mismatches 157;	Indels 7;	Gaps 1

```

OY 64 AATTAAGATACCTGGAATAGCTAGCTGTAATTAATTAAGCATATAGATTTTGGAAAT 123
Db 453 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 512
OY 124 AGTATTTGAGTTAATTAAGTATTTGAGTTGTAACAGTTTTTAATTCAGGCCCATG 183
Db 513 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 572
OY 184 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 243
Db 573 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 632
OY 244 AATCGGTAGTGTGCATATTTTCAATTTATTTTAAATTAATTAATTAATTAATTAATTAAT 303
Db 633 AATTTTWTWTWTAAATTTTTTTTTTAAKTKTTTTTTTTTTTAAATTA-----AAAA 685
OY 304 TATCGGTACAGTTATAGATTTATATTAATAATCTACGGTTCTTCAGAGAAACCTAAAAAT 363
Db 686 WTTTTAAATAAAATTTTAAAAAADAADKAAADKAAADKAAADKAAADKAAADKAAADKAAADK 745
OY 364 CGTTTCGGTGGCGACGGTTCGATCGGTTAGTCGATTTTCAAAATATTCATTTGACATCTCT 423
Db 746 KKGKKKKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGGKGG 805
OY 424 AGTGTGTGTATAGGTAAATAACCAATTTACAGA 455
Db 806 KKGKKKKKKKAAKKKAAADRTKKTWTDDAAAA 837

```

RESULT 10	CNS016LI/c	LOCUS	DEFINITION
	CNS016LI	1101 bp	DNA linear GSS 26-JUL-1999
			Drosophila melanogaster genome survey sequence T7 end of BAC
			BACN16D22 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

http://www.edg.ebi.ac.uk/. This *Prosopilia melanogaster* BAC library (Dros BAC) was made by Alain Billard at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobacII.

FEATURES	Location/Qualifiers
source	1. .1101
	/organism="Drosophila melanogaster"

	a	c	g	t	others
BASE COUNT	203	220	84	158	436
ORIGIN	.	.	.	.	.

Query Match	15.4%	Score 70.2	DB 17	Length 1101
Best Local Similarity	31.6%	Pred. No. 0.0068		
Matches 90	Conservative 84	Mismatches 11	Indels 0	Gaps 0

[illegible]

LOCUS	DEFINITION	LOCUS	DEFINITION
CNS0145P	1043 bp	CNS0145P	1043 bp
CNS0145P	Drosophila melanogaster genome survey sequence T7 end of BAC	CNS0145P	Drosophila melanogaster genome survey sequence T7 end of BAC
CNS0145P	BA0N1G11 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.	CNS0145P	BA0N1G11 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

COMMENT  
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

```
FEATURES      Location/Qualifiers
source        1..1043
              /organism="Drosophila melanogaster"
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